



TECH CENTER 1600/2909

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Table IV. HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQUENCE	SEQ ID NO:	BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	3475	25
A*0201	941.01	FLPSDYFPSV	3476	5.0
A*0202	941.01	FLPSDYFPSV	3476	4.3
A*0203	941.01	FLPSDYFPSV	3476	10
A*0206	941.01	FLPSDYFPSV	3476	3.7
A*0207	941.01	FLPSDYFPSV	3476	23
A*6802	1141.02	FTQAGYPAL	3477	40
A*0301	941.12	KVFPYALINK	3478	11
A*1101	940.06	AVDLYHFLK	3479	6.0
A*3101	941.12	KVFPYALINK	3478	18
A*3301	1083.02	STLPETYVRR	3480	29
A*6801	941.12	KVFPYALINK	3479	8.0
A*2402	979.02	AYIDNYNKF	3481	12
B*0702	1075.23	APRTLVL	3482	5.5
B*3501	1021.05	FPFKYAAAF	3483	7.2
B51	1021.05	FPFKYAAAF	3483	5.5
B*5301	1021.05	FPFKYAAAF	3483	9.3
B*5401	1021.05	FPFKYAAAF	3483	10



Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	Sequence	SEQ ID NO:	Binding Affinity (nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	3484	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	3485	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	3484	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	3486	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	3486	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	3487	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	3487	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	3487	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	3487	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	3487	20
DRB1*1201	DR5w12	1200.05	EALHQLKINPYVLS	3488	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	3489	3.5
DRB1*1501	DR2w2 β 1	507.02	GRTQDENPVVHFFKNI VTPRTPPP	3490	9.1
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	3491	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	3486	58
DRB5*0101	DR2w2 β 2	553.01	QYIKANSKFIGITE	3487	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

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TABLE VII

HBV A01 SUPER MOTIF(With binding information)

Conservancy	Freq.	Protein	Position	Sequence	SEQ ID NO:	String	A*0101
95	19	POL	521	AICSVVRRAF	1	XIXXXXXXXF	
95	19	NUC	54	ALRQAILCW	2	XLXXXXXXW	
80	16	BNV	108	AMQWNSTTF	3	XMXXXXXXF	
100	20	POL	166	ASFCGSPY	4	XSXXXXXXY	
100	20	POL	166	ASFCGSPYSW	5	XSXXXXXXW	
90	18	NUC	19	ASKLCLGW	6	XSXXXXXXW	
85	17	NUC	19	ASKLCLGWLW	7	XSXXXXXXW	
80	16	POL	822	ASPLHVAW	8	XSXXXXXXW	
100	20	BNV	312	CIPISSW	9	XIXXXXXXW	
100	20	BNV	312	CIPISSWAF	10	XIXXXXXXXF	
95	19	BNV	253	CLIFLLVLLDY	11	XLXXXXXXXXY	
95	19	BNV	239	CLRRFIIF	12	XLXXXXXXF	
75	15	BNV	239	CLRRFIIFL	13	XLXXXXXXF	
95	19	POL	523	CSVVRRAF	14	XSXXXXXXF	
100	20	BNV	310	CTCIPSSW	15	XTXXXXXXW	
90	18	NUC	31	DIDPYKEF	16	XIXXXXXX	
85	17	NUC	29	DLLDTASALY	17	XLXXXXXXXXY	11.1000
95	19	BNV	196	DSWWTSLNF	18	XSXXXXXXF	
95	19	NUC	43	ELLSFLPSDF	19	XLXXXXXXF	
95	19	NUC	43	ELLSFLPSDFF	20	XLXXXXXXF	
95	19	POL	374	ESRLVDF	21	XSXXXXXXF	
95	19	POL	374	ESRLVDFSQF	22	XSXXXXXXF	
80	16	BNV	248	FILLCLIF	23	XIXXXXXX	
80	16	BNV	246	FLFILLCLIF	24	XLXXXXXXF	
95	19	BNV	256	FLLVLLDY	25	XLXXXXXXY	
95	19	POL	658	FSPTYKAF	26	XSXXXXXXF	
90	18	X	63	FSSAGPCALRF	27	XSXXXXXXF	
100	20	BNV	333	FSWLSLVPF	28	XSXXXXXXF	
95	19	POL	656	FTFSPTYKAF	29	XTXXXXXXF	
95	19	BNV	346	FVGLSPTW	30	XVXXXXXXW	
95	19	POL	627	GLLGFAAPF	31	XLXXXXXXF	
95	19	POL	509	GLSPFLAQF	32	XLXXXXXXF	
85	17	NUC	29	GMDIDPYKEF	33	XMXXXXXXF	
95	19	NUC	123	GVWIRTPPAY	34	XVXXXXXXX	0.0017
75	15	POL	569	HLNPNKTKRW	35	XLXXXXXXW	
80	16	POL	491	HLYSHPIILGF	36	XLXXXXXXF	
85	17	POL	715	HTAELLAACF	37	XTXXXXXXF	
95	19	NUC	52	HTALRQAILCW	38	XTXXXXXXW	
100	20	POL	149	HTLWKAGILY	39	XTXXXXXXX	0.0300
100	20	BNV	249	ILLCLIF	40	XLXXXXXXF	
80	16	POL	760	ILRGTSFVY	41	XLXXXXXXX	0.0017
90	18	BNV	188	ILTIQSLDSW	42	XLXXXXXXW	
90	18	POL	625	IVGLLGFAAPF	43	XVXXXXXXF	
80	16	POL	503	KIPMGVGLSPF	44	XIXXXXXXXF	
85	17	NUC	21	KLCGLWLW	45	XLXXXXXXW	
75	15	POL	108	KLIMPARF	46	XLXXXXXXF	
75	15	POL	108	KLIMPARFY	47	XLXXXXXXX	0.0017
80	16	POL	610	KLPVNRPIDW	48	XLXXXXXXW	
85	17	POL	574	KTKRWGYSILNF	49	XTXXXXXXF	
95	19	POL	55	KVGNFTGLY	50	XVXXXXXXX	0.0680
95	19	BNV	254	LIFLLVLLDY	51	XIXXXXXXXX	0.0084
100	20	POL	109	LIMPARFY	52	XIXXXXXX	
85	17	NUC	30	LLDTASALY	53	XLXXXXXXX	25.0000
80	16	POL	752	LLGCAANW	54	XLXXXXXXW	
95	19	POL	628	LLGFAAPF	55	XLXXXXXXF	
100	20	BNV	378	LLPIFFCLW	56	XLXXXXXXW	
100	20	BNV	378	LLPIFFCLWVY	57	XLXXXXXXX	
95	19	NUC	44	LLSFLPSDF	58	XLXXXXXXF	
95	19	NUC	44	LLSFLPSDFF	59	XLXXXXXXF	
90	18	POL	407	LLSSNLSW	60	XLXXXXXXW	
95	19	BNV	175	LLVLQAGF	61	XLXXXXXXF	
95	19	BNV	175	LLVLQAGFF	62	XLXXXXXXF	
100	20	BNV	338	LLVPFQW	63	XLXXXXXXW	
100	20	BNV	338	LLVPFQWF	64	XLXXXXXXF	
85	17	NUC	100	LLWFHISCLTF	65	XLXXXXXXF	
95	19	NUC	45	LSFLPSDF	66	XSXXXXXXF	
95	19	NUC	45	LSFLPSDFF	67	XSXXXXXXF	
95	19	POL	415	LSLDVSAAF	68	XSXXXXXXF	
95	19	POL	415	LSLDVSAAFY	69	XSXXXXXXX	4.2000
100	20	BNV	336	LSLLVPFQW	70	XSXXXXXXW	
100	20	BNV	336	LSLLVPFQWF	71	XSXXXXXXF	
95	19	X	53	LSLRGLPVCAF	72	XSXXXXXXF	
95	19	POL	510	LSPFLAQF	73	XSXXXXXXF	
75	15	BNV	349	LSPTVWLSVIW	74	XSXXXXXXW	
85	17	POL	742	LSRKYTSF	75	XSXXXXXXF	
85	17	POL	742	LSRKYTSFPW	76	XSXXXXXXW	
75	15	BNV	16	LSVPNPLGF	77	XSXXXXXXF	
75	15	NUC	137	LTFGRETVLEY	78	XTXXXXXXX	
90	18	BNV	189	LTIQSLDSW	79	XTXXXXXXW	
90	18	BNV	189	LTIQSLDSWW	80	XTXXXXXXW	
90	18	POL	404	LTNLLSSNLSW	81	XTXXXXXXW	
95	19	BNV	176	LVQAGFF	82	XVXXXXXXF	
100	20	BNV	339	LVPFQWF	83	XVXXXXXXF	
100	20	POL	377	LVDFSQF	84	XVXXXXXXF	
85	17	BNV	360	MMWYWGPSLY	85	XMXXXXXXX	0.0810
75	15	X	103	MSTTDLEAY	86	XSXXXXXXX	0.8500
75	15	X	103	MSTTDLEAYF	87	XSXXXXXXF	

TABLE VII

HBV A01 SUPER MOTIF(With binding information)

Conservancy	Freq.	Protein	Position	Sequence	SEQ ID NO:	String	A*0101
95	19	POL	42	NLGNLNSIPW	88	XLXXXXXXXXXW	
90	18	POL	406	NLLSSNLSW	89	XLXXXXXXXXXW	
95	19	POL	45	NLNSVIPW	90	XLXXXXXXXXXW	
75	15	ENV	15	NLSVPNPLGF	91	XLXXXXXXXXXF	
90	18	POL	738	NSVVLRSKY	92	XSXXXXXXXXXY	0.0005
100	20	ENV	380	PIFFCLWVY	93	XIXXXXXXXXXY	0.0078
100	20	ENV	314	PIPSSWAF	94	XIXXXXXXF	
100	20	POL	124	PLDKGIKPY	95	XLXXXXXXXXXY	0.0190
100	20	POL	124	PLDKGIKPY	96	XLXXXXXXXXXY	0.1600
100	20	ENV	377	PLLPIFFCLW	97	XLXXXXXXXXXW	
95	19	ENV	174	PLLVLQAGF	98	XLXXXXXXXXXF	
95	19	ENV	174	PLLVLQAGF	99	XLXXXXXXXXXF	
80	16	POL	505	PMGVGLSPF	100	XMXXXXXXXXF	
85	17	POL	797	PTTGRTSLY	101	XTXXXXXXXXY	0.7700
75	15	ENV	351	PTVWLSVIW	102	XTXXXXXXXXXW	
85	17	POL	612	PVNRPIDW	103	XVXXXXXXXXW	
95	19	POL	685	QVFADATPTG	104	XVXXXXXXXXXW	
90	18	POL	624	RIVGLLG	105	XIXXXXXXF	
75	15	POL	106	RLKLIMPARF	106	XLXXXXXXXXXF	
75	15	POL	106	RLKLIMPARFY	107	XLXXXXXXXXXY	
95	19	POL	376	RLVDFSQF	108	XLXXXXXXXXF	
90	18	POL	353	RTPARVTGGVF	109	XTXXXXXXXXXF	
100	20	POL	49	SIPWTHKVGNF	110	XIXXXXXXXXXF	
95	19	ENV	194	SLDSWWTSLNF	111	XLXXXXXXXXXF	
95	19	POL	416	SLDVSAAF	112	XLXXXXXF	
95	19	POL	416	SLDVSAAFY	113	XLXXXXXXXXY	17.2000
100	20	ENV	337	SLVVPFVQW	114	XLXXXXXXXXW	
100	20	ENV	337	SLVVPFVQWF	115	XLXXXXXXXXXF	
95	19	X	54	SLRGLPVCAF	116	XLXXXXXXXXXF	
90	18	X	64	SSAGPCALRF	117	XSXXXXXXXXXF	
75	15	X	104	STTDLEAY	118	XTXXXXXY	
75	15	X	104	STTDLEAYF	119	XTXXXXXF	
75	15	ENV	17	SVFNPPLGF	120	XVXXXXXF	
90	18	POL	739	SVVLSRKY	121	XVXXXXXY	
85	17	POL	739	SVVLSRKYTSF	122	XVXXXXXXXXXF	
90	18	ENV	190	TIQSLDSW	123	XIXXXXXXXXXW	
90	18	ENV	190	TIQSLDSWW	124	XIXXXXXXXXXW	
100	20	POL	150	TLWKAGILY	125	XLXXXXXXXXXY	0.0017
75	15	X	105	TTDLEAYF	126	XTXXXXXF	
85	17	POL	798	TTGRTSLY	127	XTXXXXXY	
80	16	NUC	16	TVQASKLCLGW	128	XVXXXXXXXXXW	
75	15	ENV	352	TVWLSVIW	129	XVXXXXXW	
85	17	POL	741	VLSRKYTSF	130	XLXXXXXF	
85	17	POL	741	VLSRKYTSFPW	131	XLXXXXXXXXXW	
85	17	POL	740	VVLSRKYTSF	132	XVXXXXXXXXXF	
80	16	POL	759	WILRGTSF	133	XIXXXXXF	
80	16	POL	759	WILRGTSFVY	134	XIXXXXXXXXXY	0.0023
95	19	NUC	125	WIRTPPAY	135	XIXXXXXXY	
80	16	POL	751	WLLGCAANW	136	XLXXXXXW	
95	19	POL	414	WLSLDVSAAF	137	XLXXXXXF	
95	19	POL	414	WLSLDVSAAFY	138	XLXXXXXXXXXY	
100	20	ENV	335	WLSLLVPF	139	XLXXXXF	
100	20	ENV	335	WLSLLVPFVQW	140	XLXXXXXXXXXW	
85	17	NUC	26	WLWGMDIDPY	141	XLXXXXXXXXXY	0.0810
95	19	ENV	237	WMCLRRFIIF	142	XMXXXXXF	
85	17	ENV	359	WMMWYWGFS	143	XMXXXXXXXXXY	
100	20	POL	52	WTHKVGNF	144	XTXXXXF	
100	20	POL	122	YLPLDKGIKPY	145	XLXXXXXXXXXY	
90	18	NUC	118	YLVSGVW	146	XLXXXXXW	
80	16	POL	493	YSHPIILGF	147	XSXXXXXF	
85	17	POL	580	YSLNFMGY	148	XSXXXXXY	

Table VIII
HBV A02 SUPER MOTIF (With binding information)

Conservancy	Frequency	Protein	Position	Sequence	SEQID NO:	AA:	A*0201	A*0202	A*0203	A*0206	A*6802
85	17	POL	721	AACFARSRGA	149	11					
85	17	POL	431	AAMPHLLV	150	8					
80	16	POL	756	AANWILRG	151	9					
95	19	POL	632	AAPFTQCGYP	152	11					
95	19	POL	521	AICSVVRR	153	9	0.0001				
90	18	NUC	58	AICWGEL	154	8					
90	18	NUC	58	AICWGLM	155	9					
95	19	POL	642	ALMPYACI	156	9		0.0340	3.3000	0.2500	0.0470
80	16	EW	108	AMQWNTT	157	8					
75	15	X	102	AMSTTDLEA	158	9	0.0013				
95	19	POL	516	AQFTSAICSV	159	10					
95	19	POL	516	AQFTSAICSW	160	11					
95	19	POL	690	ATPTGWGL	161	8					
80	16	POL	690	ATPTGWGLA	162	9					
75	15	POL	690	ATPTGWGLAI	163	10					
95	19	POL	397	AVPNLOS	164	8					
95	19	POL	397	AVPNLOSLT	165	9	0.0001				
95	19	POL	397	AVPNLOSLTNL	166	11					
80	16	POL	755	CAANWILRG	167	10					
95	19	X	61	CAFSSAGPCA	168	10	0.0001				
95	19	X	61	CAFSSAGPCAL	169	11					
90	18	X	69	CALRTSA	170	8					
100	20	EW	312	CIPSSWA	171	9	0.0010				
80	16	EW	312	CIPSSWAF	172	11					
90	18	POL	533	CLAFSYMDDV	173	10	0.0008				
90	18	POL	533	CLAFSYMDDW	174	11					
85	17	NUC	23	CLGWLWGM	175	8					
85	17	NUC	23	CLGWLWGMDI	176	10	0.0093				
100	20	EW	253	CLIFLLV	177	8	0.0002				
100	20	EW	253	CLIFLLVL	178	9	0.0006				
95	19	EW	239	CLRRFI	179	9	0.0002				
75	15	EW	239	CLRRFI	180	11	0.0004				
90	18	NUC	107	CLTFRET	181	8					
90	18	NUC	107	CLTFRET	182	9	0.0001				
80	16	X	7	COLDPARDV	183	9					
80	16	X	7	COLDPARDVL	184	10					
85	17	POL	622	CORVGLL	185	8					
85	17	POL	622	CORVGLLGFA	186	11					
95	19	POL	684	COVFADAT	187	8					
95	19	POL	684	COVFADATPT	188	10					
100	20	EW	310	CTCIPSSWA	189	11					
95	19	POL	689	DATPTGWGL	190	9	0.0001				

Table VIII
HBV A02 SUPER MOTIF (With binding information)

Conservancy	Frequency	Protein	Position	Sequence	SEQID NO:	AA	A*0201	A*0202	A*0203	A*0206	A*6802
80	16	POL	689	DATPTGWGLA	191	10					
75	15	POL	689	DATPTGWGLAI	192	11					
90	18	NUC	31	DIDPYKEFGA	193	10					
85	17	NUC	29	DLDTASA	194	8					
85	17	NUC	29	DLDTASAL	195	9	0.0001				
95	19	POL	40	DNLGNLV	196	9	0.0004				
95	19	POL	40	DNLGNLVSI	197	11					
80	16	NUC	32	DTASALYREA	198	10					
80	16	NUC	32	DTASALYREAL	199	11					
95	19	X	14	DVLCRPV	200	8					
95	19	X	14	DVLCRPVGA	201	10	0.0001				
90	18	POL	541	DVLGAKSV	202	9	0.0003				
100	20	POL	17	EAGPLEEEL	203	9	0.0001				
80	16	X	122	ELGEEEL	204	8					
90	18	POL	718	ELLAACFA	205	8					
75	15	NUC	142	ETVLEYLV	206	8					
95	19	POL	687	FADATPTGWGL	207	11					
85	17	POL	724	FARSRSA	208	8					
80	16	POL	821	FASPLHVA	209	8					
95	19	POL	396	FAVNLQSL	210	9					
95	19	POL	396	FAVNLQSLT	211	10	0.0003				
80	16	BW	243	FIIFLFI	212	8	0.0006				
80	16	BW	243	FIIFLFI	213	9	0.0002				
80	16	BW	243	FIIFLFI	214	10	0.0012				
80	16	BW	248	FILLCL	215	8	0.0003				
80	16	BW	248	FILLCLIFL	216	10	0.0280				
80	16	BW	248	FILLCLIFL	217	11	0.0010				
80	16	BW	246	FLFILLCL	218	9	0.0002				
80	16	BW	246	FLFILLCL	219	10	0.0013				
75	15	BW	171	FLGPLVL	220	8					
75	15	BW	171	FLGPLVLQA	221	10	0.0190				
95	19	POL	513	FLLAQFSA	222	9	0.2400				
95	19	POL	513	FLLAQFSAI	223	10	0.2100	0.0320	7.0000	0.1100	0.0880
95	19	POL	562	FLSLGIHL	224	9	0.6500	0.0010	0.0100	0.1100	0.0035
80	16	BW	183	FLTRILT	225	8					
80	16	BW	183	FLTRILT	226	9	0.5100	0.0430	8.0000	0.2000	0.0010
95	19	BW	256	FLVLLDYQGM	227	11					
100	20	POL	363	FLVDKNPHNT	228	10	0.0012				
95	19	POL	656	FTFSPTYKA	229	9	0.0056	0.0150	0.0031	0.8000	7.3000
95	19	POL	656	FTFSPTYKAF	230	11					
95	19	POL	59	FTGLYSST	231	8					
90	18	POL	59	FTGLYSSTV	232	9	0.0005				

HBV A02 SUPER MOTIF (With binding information)

Table VIII

Conservancy	Frequency	Protein	Position	Sequence	SEQ ID NO:	AA	A*0201	A*0202	A*0203	A*0206	A*6802
95	19	POL	635	FTQCGYP	233	8					
95	19	POL	635	FTQCGYPAL	234	9	0.0009				
95	19	POL	635	FTQCGYPALM	235	10	0.0024				
95	19	POL	518	FTSAICSV	236	8					
95	19	POL	518	FTSAICSVV	237	9	0.0090				
95	19	BW	346	FVGLSPTV	238	8					
95	19	BW	346	FVGLSPTVWL	239	10	0.0008				
90	18	X	132	FVLGGRHKL	240	10	0.0030				
90	18	X	132	FVLGGRHKL	241	11					
95	19	BW	342	FVQWVGL	242	8					
95	19	BW	342	FVQWVGLSPT	243	11					
90	18	POL	766	FVYVPSAL	244	8					
90	18	POL	766	FVYVPSALNPA	245	11					
95	19	X	50	GAHLSLRL	246	9	0.0001				
90	18	X	50	GAHLSLRLPLV	247	11					
85	17	POL	545	GAKSVOHL	248	8					
85	17	POL	545	GAKSVOHLES	249	11					
75	15	POL	567	GIHLPNKT	250	9					
90	18	POL	155	GILYKRET	251	8					
90	18	POL	155	GILYKRETT	252	9					
85	17	POL	682	GLCQVFADA	253	9	0.0024				
85	17	POL	682	GLCQVFADAT	254	10					
95	19	POL	627	GLLGFAAPT	255	10					
85	17	BW	62	GLLGWSPOA	256	9	0.0049	0.0003	0.0350	0.2800	0.0005
95	19	X	57	GLPVCAFSSA	257	10	0.4000				
95	19	POL	509	GLSPFLA	258	8	0.0008				
95	19	POL	509	GLSPFLAQFT	259	11					
100	20	BW	348	GLSPTWL	260	8	0.0036				
75	15	BW	348	GLSPTWLSV	261	10	0.2800				
75	15	BW	348	GLSPTWLSVI	262	11	0.0036				
90	18	BW	265	GMLPVCP	263	8					
90	18	POL	735	GTDNSWL	264	8					
75	15	BW	13	GTNLSVPNPL	265	10					
80	16	POL	763	GTSFYVPSA	266	10					
80	16	POL	763	GTSFYVPSAL	267	11					
80	16	POL	507	GVGLSPFL	268	8					
80	16	POL	507	GVGLSPFL	269	9	0.0002				
80	16	POL	507	GVGLSPFLA	270	10					
95	19	NUC	123	GWIRTPPA	271	9	0.0030				
90	18	NUC	104	HISLTFGRET	272	11					
80	16	POL	435	HLLVGSSGL	273	9	0.0031				
90	18	X	52	HLSLRLPLV	274	9	0.0014				

HBV A02 SUPER MOTIF (With binding information)

Table VIII

Conservancy	Frequency	Protein	Position	Sequence	SEQ ID NO:	AA	A*0201	A*0202	A*0203	A*0206	A*6802
90	18	X	52	HLSRLGPLVCA	275	11					
80	16	POL	491	HLVSHPII	276	8					
80	16	POL	491	HLVSHPII	277	9	0.2200	0.0003	0.9300	0.1700	0.0530
85	17	POL	715	HTAELLAA	278	8					
85	17	POL	715	HTAELLAA	279	11					
100	20	NUC	52	HTALROAI	280	8					
95	19	NUC	52	HTALROAIL	281	9	0.0001				
100	20	POL	149	HTLWKAGI	282	8					
100	20	POL	149	HTLWKAGIL	283	9	0.0001				
80	16	ENV	244	IILFILL	284	8	0.0004				
80	16	ENV	244	IILFILL	285	9	0.0002				
80	16	ENV	244	IILFILLCL	286	11	0.0002				
80	16	POL	497	IILGFRKI	287	8					
80	16	POL	497	IILGFRKIPM	288	10					
90	18	NUC	59	ILCWGELM	289	8					
80	16	POL	498	ILGFRKIPM	290	9	0.0002				
100	20	ENV	249	ILLICUFL	291	9	0.0015				
100	20	ENV	249	ILLICUFL	292	10	0.0190	0.0001	0.0002	0.1300	0.0015
100	20	ENV	249	ILLICUFLV	293	11	0.0056				
80	16	POL	760	ILRGTSFV	294	8					
80	16	POL	760	ILRGTSFVYV	295	10	0.0160				
100	20	NUC	139	ILSTLPET	296	8					
100	20	NUC	139	ILSTLPETT	297	9	0.0001				
100	20	NUC	139	ILSTLPETT	298	10	0.0210	0.0085	0.0770	0.3100	0.0067
100	20	NUC	139	ILSTLPETT	299	11					
95	19	ENV	188	ILTIQSL	300	8					
90	18	POL	156	ILYKRETT	301	8					
90	18	POL	625	IVGLLGFA	302	8					
90	18	POL	625	IVGLLGFAA	303	9	0.0009				
90	18	POL	153	KAGILYKRET	304	10					
90	18	POL	153	KAGILYKRETT	305	11					
80	16	POL	503	KIPMGVGL	306	8					
85	17	NUC	21	KLCGLWLWGM	307	10					
95	19	POL	489	KLHLYSHPI	308	9	0.0001	0.0340	2.7000	0.5900	0.0015
80	16	POL	489	KLHLYSHPII	309	10	0.0690				
80	16	POL	489	KLHLYSHPII	310	11					
80	16	POL	610	KLPVNRPI	311	8					
95	19	POL	653	KQAFIFSPT	312	9					
95	19	POL	574	KTKRWGYSL	313	9	0.0001				
85	17	POL	620	KVCQRVGL	314	9	0.0003				
85	17	POL	620	KVCQRVGLL	315	10	0.0001				
95	19	POL	55	KVGNFTGL	316	8					

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Table VIII

Conservancy	Frequency	Protein	Position	Sequence	SEQ ID NO:	AA	A*0201	A*0202	A*0203	A*0206	A*6802
85	17	X	91	KVLHKRTL	317	8					
85	17	X	91	KVLHKRTLGL	318	10					
90	18	POL	534	LAFSYMDDV	319	9	0.0004				
90	18	POL	534	LAFSYMDDV	320	10	0.0002				
90	18	POL	534	LAFSYMDDVWL	321	11	0.0003				
95	19	POL	515	LAQFTSAI	322	8					
95	19	POL	515	LAQFTSAICSV	323	11					
100	20	EW	254	LIFLLVLL	324	8	0.0025				
95	19	POL	514	LLAQFTSA	325	8					
95	19	POL	514	LLAQFTSAI	326	9	0.1000	0.2700	3.7000	0.2600	0.7900
100	20	EW	251	LLCLIFLL	327	8	0.0004				
100	20	EW	251	LLCLIFLLV	328	9	0.0048				
100	20	EW	251	LLCLIFLLVL	329	10	0.0075				
100	20	EW	251	LLCLIFLLVLL	330	11	0.0013				
85	17	NJC	30	LLDTASAL	331	8					
95	19	EW	260	LLDYQGML	332	8	0.0004				
90	18	EW	260	LLDYQGMPLV	333	10	0.0980	0.0001	0.0200	0.6700	0.0009
80	16	POL	752	LLGCAANWI	334	9	0.0011				
80	16	POL	752	LLGCAANWIL	335	10	0.0140				
95	19	POL	628	LLGFAAPT	336	9	0.0008				
85	17	EW	63	LLGWSPQA	337	8					
75	15	EW	63	LLGWSPQAQGI	338	11					
100	20	EW	250	LLCLIFL	339	8	0.0006				
100	20	EW	250	LLCLIFLL	340	9	0.0065				
100	20	EW	250	LLCLIFLLV	341	10	0.0036				
100	20	EW	250	LLCLIFLLVL	342	11	0.0005				
100	20	EW	378	LLPIFFCL	343	8	0.0055				
100	20	EW	378	LLPIFFCLWV	344	10	0.0320	0.0008	0.0150	0.8000	0.0005
95	19	POL	563	LLSLGIHL	345	8					
90	18	POL	407	LLSSNLSWL	346	9	0.0110	0.0780	3.9000	0.2700	0.0100
90	18	POL	407	LLSSNLSWLSL	347	11					
80	16	EW	184	LLTRILTI	348	8	0.0026				
80	16	POL	436	LLVGSSGL	349	8					
95	19	EW	257	LLVLDYQGM	350	10	0.0050				
95	19	EW	257	LLVLDYQGMVL	351	11					
90	18	EW	175	LLVLOAGFFL	352	10	0.0310	0.0037	0.0045	0.1500	0.0110
90	18	EW	175	LLVLOAGFFLL	353	11	0.0074				
95	19	EW	338	LLVPRVQWIFV	354	10	0.6700	0.3800	1.7000	0.2900	0.1400
90	18	NJC	100	LLWFHISCL	355	9	0.0130	0.0002	0.0420	0.3100	0.0098
85	17	NJC	100	LLWFHISCLT	356	10					
95	19	POL	643	LMPLYACI	357	8					
95	19	EW	178	LOAGFFLL	358	8					

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Table VIII

Conservancy	Frequency	Protein	Position	Sequence	SEQID NO:	AA	A*0201	A*0202	A*0203	A*0206	A*6802
95	19	BW	178	LOAGFLLT	359	9					
80	16	BW	178	LOAGFLLTRI	360	11					
100	20	POL	401	LOSLTNLL	361	8					
95	19	NUC	108	LTFGRETV	362	8					
75	15	NUC	137	LTFGRETVL	363	9					
90	18	POL	404	LTNLLSNL	364	9					
80	16	BW	185	LTRLTIQSL	365	11					
85	17	POL	99	LTVNEKRRL	366	9					
100	20	POL	364	LVDKNPHNT	367	9	0.0001				
95	19	BW	258	LVLDDYQGM	368	9	0.0001				
95	19	BW	258	LVLDDYQGMIL	369	10	0.0001				
90	18	BW	176	LVLQAGFLL	370	9	0.0096				
90	18	BW	176	LVLQAGFLL	371	10	0.0022				
90	18	BW	176	LVLQAGFLLT	372	11					
95	19	BW	339	LVPFQWVF	373	9	0.0420	0.0150	0.0048	0.7900	2.8000
95	19	BW	339	LVPFQWVF/GL	374	11					
90	18	NUC	119	LVSFGWII	375	8	0.0004				
90	18	NUC	119	LVSFGWIRT	376	10					
85	17	BW	360	MMWYWGPSL	377	9	0.6400				
75	15	NUC	1	MLFHLCL	378	8					
100	20	NUC	136	NAPILSTL	379	8					
100	20	NUC	136	NAPILSTLPET	380	11					
95	19	POL	42	NILGNLWSI	381	9	0.0047				
90	18	POL	406	NILSSNLSWL	382	10	0.0016				
95	19	POL	45	NLNVSIPIWT	383	9	0.0005				
100	20	POL	400	NLQSLTNL	384	8					
100	20	POL	400	NLQSLTNLL	385	9					
75	15	BW	15	NLSVNPPL	386	8					
90	18	POL	411	NLSWLSLDV	387	9	0.0650	0.0051	0.6400	0.1600	0.0990
90	18	POL	411	NLSWLSLDVSA	388	11					
100	20	POL	47	NVSIPIWTHKV	389	10	0.0001				
100	20	POL	430	PAAMPPLL	390	8					
85	17	POL	430	PAAMPPLL	391	9					
90	18	POL	775	PADDPGRGL	392	10					
90	18	BW	131	PAGSSSGT	393	9					
90	18	BW	131	PAGSSSGTV	394	10					
95	19	POL	641	PALMPLYA	395	8					
95	19	POL	641	PALMPLYACI	396	10	0.0001				
75	15	X	145	PAPCNFTT	397	8					
75	15	X	145	PAPCNFTTSA	398	10					
80	16	X	11	PARDVLCL	399	8					
75	15	X	11	PARDVLCRLPV	400	11					

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Table VIII

Conservancy	Frequency	Protein	Position	Sequence	SEQID NO:	AA	A*0201	A*0202	A*0203	A*0206	A*6802
90	18	POL	355	PARVTGGV	401	8					
90	18	POL	355	PARVTGGVFL	402	10					
90	18	POL	355	PARVTGGVFLV	403	11					
95	19	NUC	130	PAYRPPNA	404	8					
95	19	NUC	130	PAYRPPNAPI	405	10	0.0001				
95	19	NUC	130	PAYRPPNAPIL	406	11					
85	17	POL	616	PIDWKVCORI	407	10	0.0001				
85	17	POL	616	PIDWKVCORIV	408	11					
100	20	EW	380	PIFFCLWV	409	8					
100	20	EW	380	PIFFCLWVYI	410	10	0.0004				
85	17	POL	713	PIHTAELL	411	8					
85	17	POL	713	PIHTAELLA	412	9					
80	16	POL	496	PIILGFRKI	413	10					
80	16	POL	496	PIILGFRKIPM	414	9	0.0001				
100	20	NUC	138	PILSTLPET	415	11					
100	20	NUC	138	PILSTLPETT	416	9	0.0001				
100	20	NUC	138	PILSTLPETTV	417	10	0.0001				
80	16	EW	314	PIPSSWAF	418	11	0.0001				
95	19	POL	20	PLEELPRL	419	9					
90	18	POL	20	PLEELPRLA	420	9	0.0003				
95	19	EW	10	PLGFFPDHQL	421	10	0.0001				
100	20	POL	427	PLHPAAMPHL	422	10	0.0002				
100	20	POL	427	PLHPAAMPHLL	423	10	0.0001				
100	20	EW	377	PLLPFFCL	424	11					
100	20	EW	377	PLLPFFCLW	425	9	0.0650	0.0001	0.0018	0.1100	0.0047
90	18	EW	174	PLLVQAGFL	426	11					
80	16	POL	711	PLPIHTAEL	427	11	0.0008				
80	16	POL	711	PLPIHTAELL	428	9	0.0004				
80	16	POL	711	PLPIHTAELLA	429	10	0.0001				
75	15	POL	2	PLSYQHFRKL	430	11					
75	15	POL	2	PLSYQHFRKLL	431	10	0.0001				
85	17	POL	98	PLTVNEKRRL	432	11					
80	16	POL	505	PMGVGLSPFL	433	10	0.0001				
80	16	POL	505	PMGVGLSPFL	434	10	0.0001				
95	19	EW	106	POAMQWNST	435	11					
80	16	EW	106	POAMQWNSTT	436	9					
90	18	EW	192	POSLSWSWT	437	10					
90	18	EW	192	POSLSWSWTSL	438	9					
75	15	POL	692	PTGWGLAI	439	11					
80	16	EW	219	PTSNHSPT	440	8					
85	17	POL	797	PTTGRTSL	441	8					
					442	8					

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Table VIII

Conservancy	Frequency	Protein	Position	Sequence	SEQID NO.	AA	A*0201	A*0202	A*0203	A*0206	A*6802
85	17	POL	797	PTGRTSLYA	443	10					
80	16	NUC	15	PTVOASKL	444	8					
80	16	NUC	15	PTVQASKLCL	445	10					
75	15	BN	351	PTVWLSVI	446	8					
75	15	BN	351	PTVWLSVIWM	447	10					
95	19	X	59	PVCAFFSA	448	8					
85	17	POL	612	PVNRPIDWKV	449	10	0.0002				
95	19	POL	654	QAFIFSPT	450	8					
95	19	POL	654	QAFIFSPTYKA	451	11					
95	19	BN	179	QAGFFLT	452	8					
80	16	BN	179	QAGFFLTRI	453	10					
80	16	BN	179	QAGFFLTRIL	454	11					
90	18	NUC	57	QAILCWGEL	455	9					
90	18	NUC	57	QAILCWGELM	456	10					
95	19	BN	107	QAMQWNST	457	8					
80	16	BN	107	QAMQWNSTT	458	9					
80	16	NUC	18	QASKLCGLWL	459	10					
80	16	X	8	QLDPADV	460	8	0.0001				
80	16	X	8	QLDPADVCL	461	9	0.0001				
80	16	X	8	QLDPADVCLCL	462	11	0.0001				
90	18	NUC	99	QLLWFHISCL	463	10	0.0060				
85	17	NUC	99	QLLWFHISCLT	464	11					
95	19	POL	685	QVFADATPT	465	9	0.0001				
95	19	POL	528	RAFPHCLA	466	8					
80	16	BN	187	RILTIQSL	467	9	0.0010				
90	18	POL	624	RIVGLLGFA	468	9					
90	18	POL	624	RIVGLLGFAA	469	10					
75	15	POL	106	RLKLIMPA	470	8					
90	18	NUC	56	ROALCWGEL	471	10					
90	18	NUC	56	ROALCWGELM	472	11					
90	18	NUC	98	ROLLWFI	473	8					
90	18	NUC	98	ROLLWFHISCL	474	11					
85	17	BN	88	QSGROPT	475	8					
90	18	POL	353	RTPARVTGGV	476	10					
95	19	NUC	127	RTPPAYRPPNA	477	11					
95	19	POL	36	RVAEDNL	478	8					
90	18	POL	36	RVAEDNLGNL	479	11					
80	16	POL	818	RVHFASPL	480	8					
75	15	POL	818	RVHFASPLHV	481	10	0.0001				
75	15	POL	818	RVHFASPLHVA	482	11					
100	20	POL	357	RVTGGVFL	483	8					
100	20	POL	357	RVTGGVFLV	484	9	0.0041				

Table VIII
HBV A02 SUPER MOTIF (With binding information)

Conservancy	Frequency	Protein	Position	Sequence	SEQ ID NO:	AA	A*0201	A*0202	A*0203	A*0206	A*6802
90	18	X	65	SAGPCALRFT	485	10					
95	19	POL	520	SAICSVVRRRA	486	10	0.0001				
90	18	NUC	35	SALYREAL	487	8					
100	20	POL	49	SIPWTHKV	488	8					
95	19	BW	194	SLDSWWTSL	489	9					
75	15	POL	565	SLGIHLNPKT	490	11					
95	19	BW	337	SLLVPRVQWIFV	491	11					
75	15	POL	581	SLNFMGYV	492	8					
75	15	POL	581	SLNFMGYVI	493	9	0.0038				
95	19	X	54	SLRGLPVCA	494	9	0.0007				
90	18	POL	403	SLTNLLSSNL	495	10	0.0014				
75	15	BW	216	SQSPTSNSHPT	496	11					
75	15	BW	280	STGPKCTCT	497	9					
100	20	NUC	141	STLPETTV	498	8					
100	20	NUC	141	STLPETTV	499	9	0.0019				
80	16	BW	85	STNRSRGROPT	500	11					
85	17	POL	548	SVQHLES	501	8					
80	16	BW	330	SVRFSWLSL	502	9	0.0001				
80	16	BW	330	SVRFSWLSLL	503	10	0.0004				
80	16	BW	330	SVRFSWLSLLV	504	11					
90	18	POL	739	SVLSRKYT	505	9					
95	19	POL	524	SVRRAPFHL	506	11					
85	17	POL	716	TAELLAACFA	507	10					
95	19	NUC	53	TALROAIL	508	8					
80	16	NUC	33	TASALYREA	509	9					
80	16	NUC	33	TASALYREAL	510	10					
90	18	BW	190	TIQSIDSWWT	511	11					
100	20	NUC	142	TLPETTV	512	8					
100	20	POL	150	TLWKAGIL	513	8					
95	19	POL	636	TOCGYPAL	514	8					
95	19	POL	636	TOCGYPALM	515	9					
95	19	POL	636	TOCGYPALMPL	516	11					
85	17	POL	798	TTGRTSLYA	517	9					
75	15	BW	278	TTSTGPKCT	518	9					
75	15	BW	278	TTSTGPKCTCT	519	11					
85	17	POL	100	TVNEKRRL	520	8					
80	16	NUC	16	TVQASKLCL	521	9	0.0002				
75	15	BW	352	TVWLSVINM	522	9	0.0002				
95	19	POL	37	VAEDNLGNL	523	10	0.0001				
95	19	X	15	VLCLRPVGA	524	9	0.0014				
85	17	POL	543	VLGAKSVQHL	525	10	0.0001				
90	18	X	133	VLGGRHKL	526	9	0.0009				

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Table VIII

Conservancy	Frequency	Protein	Position	Sequence	SEQ ID NO:	AA	A*0201	A*0202	A*0203	A*0206	A*6802
90	18	X	133	VLGGRHKLV	527	10	0.0001				
85	17	X	92	VLHKRTLGL	528	9	0.0012				
95	19	BN	259	VLDYQGM	529	8					
95	19	BN	259	VLDYQGM	530	9	0.0440	0.0001	0.0210	0.9000	0.0002
90	18	BN	259	VLDYQGMPLV	531	11	0.5800	0.2200	4.9000	0.3400	0.0170
95	19	BN	177	VLOAGFLL	532	8	0.0019				
95	19	BN	177	VLOAGFLL	533	9	0.0660				
95	19	BN	177	VLOAGFLLT	534	10	0.0011				
80	16	NUC	17	VOASKLCL	535	8					
80	16	NUC	17	VOASKLCLGWL	536	11					
95	19	BN	343	VQWVGLSPT	537	10					
95	19	BN	343	VQWVGLSPTV	538	11					
100	20	POL	358	VTGGVRLV	539	8					
90	18	POL	542	VLGAKSV	540	8					
80	16	POL	542	VLGAKSVQHL	541	11					
90	18	POL	740	WLSRKYT	542	8					
95	19	POL	525	WRRAPPHCL	543	10	0.0003				
95	19	POL	525	WRRAPPHCLA	544	11					
80	16	POL	759	WILRGTSFV	545	9	0.0270				
80	16	POL	759	WILRGTSFVY	546	11					
80	16	POL	751	WLLGCAANWI	547	10	0.0053				
80	16	POL	751	WLLGCAANWIL	548	11					
100	20	POL	414	WLSLDVSA	549	8					
95	19	POL	414	WLSLDVSAA	550	9	0.0059				
100	20	BN	335	WLSLLVPV	551	9	1.1000	0.0380	7.2000	0.3600	0.0310
95	19	BN	237	WMCLRRFI	552	8					
95	19	BN	237	WMCLRRFI	553	9	0.0005				
95	19	BN	237	WMCLRRFI	554	11	0.0019				
85	17	BN	359	WMWVWGPSL	555	10	0.0009				
100	20	POL	52	WTHKVGNT	556	9	0.0001				
95	19	POL	52	WTHKVGNTGL	557	11					
100	20	POL	147	YLHLWKA	558	8					
100	20	POL	147	YLHLWKAGI	559	10	0.0160	0.0005	0.5600	0.1000	0.0320
100	20	POL	147	YLHLWKAGIL	560	11					
100	20	POL	122	YPLDKGI	561	8					
90	18	NUC	118	YLVSGVWI	562	9	0.3800				
90	18	NUC	118	YLVSGVWIRT	563	11					
90	18	POL	538	YMDDVWLG	564	9	0.0250	0.0001	0.0024	0.1000	0.0002
90	18	BN	263	YQGMPLVCPL	565	10					
75	15	POL	5	YQHFRKLL	566	8					
75	15	POL	5	YQHFRKLL	567	9					
75	15	POL	5	YQHFRKLL	568	10					

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Table VIII

Conservancy	Frequency	Protein	Position	Sequence	SEQ ID NO:	AA	A*0201	A*0202	A*0203	A*0206	A*6802
85	17	POL	746	YTSFPWLL	569	8					
75	15	POL	746	YTSFPWLLGCA	570	11					
90	18	POL	768	YVPSALNPA	571	9	0.0039				

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Table IX

Conservancy	Frequency	Protein	Position	Sequence	P2	C-term	AA	A*0301	A*1101	A*3101	A*3301	A*6801	SEQID NO:
85	17	POL	721	AACFARSR	A	R	8	0.0004	0.0003	0.0056	0.0035	0.0014	572
95	19	POL	521	AICSVRR	I	R	8	-0.0002	0.0003	0.0014	-0.0009	0.0006	573
90	18	POL	772	ALNPADPSR	L	R	10	0.0003	0.0001				574
85	17	X	70	ALRFTSAR	L	R	8	0.0047	0.0009	0.0450	0.0230	0.0004	575
80	16	POL	822	ASPLHVAWR	S	R	9						576
75	15	BW	84	ASTNROSGR	S	R	9	0.0009	0.0002	0.0088	0.0008	0.0001	577
80	16	POL	755	CAANWILR	A	R	8						578
85	17	X	69	CALRFTSAR	A	R	9	0.0034	0.0230	1.5000	8.0000	0.7300	579
90	18	X	17	CLRPVGAESR	L	R	10	0.0011	0.0001				580
100	20	NUC	48	CSPHTALR	S	R	9	0.0029	0.0001	0.0520	0.0250	0.0440	581
85	17	NUC	29	DLLDTASALYR	L	R	11	0.0042	-0.0003	-0.0012	3.7000	0.0410	582
85	17	NUC	32	DTASALYR	T	R	8	0.0004	-0.0002	-0.0009	0.0018	0.0009	583
95	19	POL	17	EAGPLEEPLR	A	R	11	-0.0009	-0.0003	-0.0012	0.0015	0.0110	584
90	18	POL	718	ELLAACFAR	L	R	9	0.0002	0.0004				585
85	17	POL	718	ELLAACFARSR	L	R	11	0.0062	0.0016	0.0200	0.2000	0.1600	586
95	19	NUC	174	ETTVRRR	T	R	8	0.0003	-0.0002	-0.0009	0.1400	0.0027	587
80	16	NUC	174	ETTVRRGR	T	R	10	0.0003	0.0001				588
80	16	POL	821	FASPLHVAWR	A	R	10						589
90	18	X	63	FSSAGPCALR	S	R	10						590
95	19	POL	656	FTFSPTYK	T	K	8	0.0100	0.0100	0.0023	0.2100	0.0590	591
95	19	POL	518	FTSAICSVWR	T	R	10	0.0003	0.0003				592
95	19	POL	518	FTSAICSVVRR	T	R	11	0.0065	0.0092	0.0170	0.0350	1.5000	593
90	18	X	132	FVLGGCRHK	V	K	9	0.0430	0.0090				594
95	15	POL	567	GIHLNPNK	I	K	8						595
75	15	POL	567	GIHLNPNKTK	I	K	10	0.0025	0.0011	0.0009	0.0009	0.0003	596
75	15	POL	567	GIHLNPNKTKR	I	R	11						597
85	17	NUC	29	GMDIDPYK	M	K	8	0.0006	0.0004	-0.0009	-0.0009	0.0001	598
90	18	POL	735	GTDSNVLSR	T	R	10	0.0010	0.0420	0.0030	0.0019	0.0008	599
90	18	POL	735	GTDSNVLSRK	T	K	11	0.0140	0.5600	-0.0002	-0.0006	0.0001	600
95	19	NUC	123	GWIRTPPAYR	V	R	11	0.1900	0.1700	6.8000	0.7300	0.6600	601
90	18	NUC	104	HISCLTFGR	I	R	9	0.0160	0.0065				602
75	15	POL	569	HILNPNKTK	L	K	8						603
75	15	POL	569	HILNPNKTKR	L	R	9	0.0025	0.0001				604
100	20	POL	149	HTLWKAGILYK	T	K	11	0.5400	0.4400	0.0370	0.0720	0.1900	605
90	18	NUC	105	ISCLTFGR	S	R	8	0.0004	0.0002	0.0017	-0.0009	0.0017	606
100	20	POL	153	KAGILYKR	A	R	8	0.0002	-0.0002	0.0015	-0.0009	0.0001	607
80	16	POL	610	KLPVNRIDWK	L	K	11						608
75	15	X	130	KVPLGGCR	V	R	9	0.0420	0.0820	0.6000	0.0710	0.0030	609
85	17	POL	720	LAACFARSR	A	R	9	0.0058	0.0065				610
90	18	POL	719	LLAACFAR	L	R	8	0.0024	0.0003	0.0015	0.0029	0.0064	611
85	17	POL	719	LLAACFARSR	L	R	10						612
85	17	NUC	30	LLDTASALYR	L	R	10						613
80	16	POL	752	LLGCAANWILR	L	R	11	0.0050	0.0002				614
75	15	POL	564	LSLGIHLNPNK	S	K	11						615
95	19	NUC	169	LSTLPETTVR	S	R	11	-0.0009	0.0008	-0.0012	-0.0023	0.0078	616
75	15	POL	3	LSYQHFFK	S	K	8						617
85	17	POL	99	LTVNEKRR	T	R	8	-0.0002	-0.0002	-0.0009	-0.0009	0.0001	618
100	20	NUC	119	LVSFGWIR	V	R	9	0.0028	0.0120				619
100	20	POL	377	LWDFDSQFSR	V	R	10	0.0016	0.3600	0.0260	0.2300	0.4900	620
75	15	X	103	MSTDLWAYFK	S	K	11						621
90	18	NUC	75	NLEDPASR	L	R	8	-0.0002	-0.0002	-0.0009	-0.0009	0.0001	622

HBV A03 SUPER MOTIF (With binding information)

Table IX

Conservancy	Frequency	Protein	Position	Sequence	P2	C-term	AA	A*0301	A*1101	A*3101	A*3301	A*6801	SEQID NO:
95	19	POL	45	NLNVPWTHK	L	K	11	-0.0009	0.0005	-0.0012	-0.0023	0.0019	623
90	18	POL	738	NSVLSRK	S	K	8	0.0006	0.0010	-0.0009	-0.0009	0.0007	624
100	20	POL	47	NVSIPTWK	V	K	9	0.0820	0.0570	0.0002	0.0100	0.0320	625
90	18	POL	775	PADDPGR	A	R	9	0.0008	0.0002	0.0004	0.0015	0.0002	626
80	16	X	11	PARVLCRL	A	R	9	0.0002	0.0002	0.0100	0.0180	0.0002	627
75	15	EW	83	PASTNROSGR	A	R	10	0.0002	0.0005				628
90	18	POL	616	PIDWKVCR	I	R	9	0.0002	0.0005				629
80	16	POL	496	PILGRK	I	K	8						630
95	19	POL	20	PLEELPR	L	R	8	0.0002	-0.0002	-0.0009	-0.0009	0.0001	631
100	20	POL	2	PLSYQHR	L	R	8	-0.0002	-0.0002	-0.0009	-0.0009	0.0001	632
75	15	POL	2	PLSYQHRK	L	K	9	0.0011	0.0031	0.0005	0.0008	0.0002	633
85	17	POL	98	PLTVNEKR	L	R	8	0.0002	-0.0002	-0.0009	-0.0009	0.0001	634
85	17	POL	98	PLTVNEKR	L	R	9	0.0008	0.0005	0.0004	0.0027	0.0002	635
90	18	X	20	PVGAESGR	V	R	9	0.0002	0.0005	0.0004	0.0043	0.0002	636
85	17	POL	612	PVNRPIDWK	V	K	9	0.0310	0.1400	0.0002	0.0006	0.0009	637
95	19	POL	654	QAFISPTYK	A	K	10	0.0450	0.5400	0.0010	0.0057	1.2000	638
80	16	EW	179	QAGFLLTR	A	R	9						639
75	15	NUC	169	QSPRRRSQSR	S	R	11						640
80	16	POL	189	OSSGILSR	S	R	8	0.0950	0.0002	3.1000	0.0490	0.0002	641
75	15	POL	106	RLKIMPAR	L	R	9						642
75	15	X	128	RLKVFVGGR	L	R	11	0.2800	3.8000	2.6000	1.2000	6.1000	643
95	19	POL	376	RLWDFQFSR	L	R	11	-0.0007	-0.0003	0.0190	-0.0023	0.0003	644
95	19	NUC	183	RSPRRTPSPR	S	R	11						645
75	15	NUC	167	RSQSPRRR	S	R	8						646
75	15	NUC	167	RSQSPRRR	S	R	9						647
95	19	NUC	188	RTPSPRRR	T	R	8	-0.0002	-0.0002	0.0033	0.0014	0.0002	648
95	19	NUC	188	RTPSPRRR	T	R	9	0.0054	0.0005	0.2000	0.0016	0.0003	649
100	20	POL	357	RVTGGVFLVDK	V	K	11	0.0190	0.0290	-0.0002	-0.0003	0.0001	650
90	18	X	65	SAGPCALR	A	R	8	-0.0002	0.0020	0.0029	0.0024	0.0360	651
95	19	POL	520	SAICSVRR	A	R	8	-0.0002	0.0071	0.0280	0.0081	0.0690	652
95	19	POL	520	SAICSVRR	A	R	9	0.0058	0.2100	0.1500	0.0650	0.3800	653
90	18	POL	771	SALNPADDPSPR	A	R	11	-0.0004	-0.0003	-0.0012	-0.0023	0.0003	654
75	15	POL	565	SLGIHLNPNK	L	K	10						655
90	18	X	64	SSAGPCALR	S	R	9	0.0080	0.1400	0.3300	0.1600	0.7500	656
95	19	NUC	170	STLPETTVRR	T	R	10	0.0007	0.0600	0.0080	0.0240	0.0250	657
95	19	NUC	170	STLPETTVRR	T	R	11	0.0150	1.4000	0.1000	0.1600	0.3100	658
80	16	EW	85	STNRQSGR	T	R	8						659
75	15	X	104	STIDLEAVFK	T	K	10	0.0066	2.7000				660
85	17	POL	716	TAELLAACFAR	A	R	11	0.0006	0.0023	0.0066	0.1600	0.0590	661
95	19	NUC	171	TLPETTVRR	L	R	9	0.0008	0.0002	0.0009	0.0024	0.0180	662
95	19	NUC	171	TLPETTVRR	L	R	10	0.0007	0.0230	0.0006	0.0120	0.0440	663
95	19	NUC	171	TLPETTVRR	L	R	11	0.0005	0.0160	0.0061	0.0710	0.6400	664
100	20	POL	150	TLWKAGILYK	L	K	10	5.3000	0.3600	0.0051	0.0010	0.0130	665
100	20	POL	150	TLWKAGILYKR	L	R	11	0.0082	0.0095	0.1000	0.1100	0.0640	666
95	19	POL	519	TSACISVRR	S	R	9	0.0005	0.0008	0.0600	0.0200	0.0820	667
95	19	POL	519	TSACISVRR	S	R	10	0.0018	0.0006	0.0030	0.0066	0.0048	668
75	15	X	105	TTDLEAVFK	T	K	9	0.0006	0.9200	0.0006	0.0012	0.0170	669
75	15	EW	278	TTSTGPCK	T	K	8						670
80	16	NUC	175	TVVRRGR	T	R	9	0.0008	0.0005	0.2500	0.1400	0.0095	671
80	16	NUC	176	TVVRRGR	V	R	8	0.0003	0.0001				672
80	16	NUC	176	TVVRRGRSPR	V	R	11						673

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Table IX

Conservancy	Frequency	Protein	Position	Sequence	P2	C-term	AA	A*0301	A*1101	A*3101	A*3301	A*6801	SEQID NO:
90	18	X	133	VLGGCRHK	L	K	8	0.0150	0.0002	-0.0005	-0.0009	0.0001	674
80	16	BN	177	VLOAGFFLTR	L	R	11						675
90	18	NUC	120	VSGWIR	S	R	8	0.0040	0.0290	0.0750	0.0270	0.0360	676
100	20	POL	48	VSPWTHK	S	K	8	0.0130	0.0170	0.0031	0.0013	0.0004	677
100	20	POL	358	VTGGVFLVK	T	K	10	0.0390	0.0920	0.0002	0.0006	0.0022	678
100	20	POL	378	WDFSQFSR	V	R	9	0.0015	0.0750	0.0013	0.0170	0.0330	679
80	16	NUC	177	WRRGRSPR	V	R	10	0.0027	0.0001				680
80	16	NUC	177	WRRGRSPRR	V	R	11						681
95	19	NUC	125	WIRTPAYR	I	R	9	0.0008	0.0005				682
90	18	POL	314	WLQFRNSK	L	K	8	-0.0002	0.0005	0.0020	0.0052	0.0001	683
85	17	NUC	26	WLWGMIDIPYK	L	K	11	0.0030	0.0013	-0.0003	0.0039	0.0490	684
100	20	POL	122	YLPDKGIK	L	K	9	0.0001	0.0001	0.0006	0.0006	0.0002	685
90	18	NUC	118	YLVSGWIR	L	R	10	0.0005	0.0002				686
90	18	POL	538	YMDDVLGAK	M	K	10	0.0330	0.0043	0.0002	0.0006	0.0001	687
80	16	POL	493	YSHPIIGFR	S	R	10						688
80	16	POL	493	YSHPIIGFRK	S	K	11						689

Table X

HBV A24 SUPER MOTIF (With binding information)

Conservancy	Freq	Protein	Position	Sequence	String	A*2401	SEQ ID NO:
95	19	POL	529	AFPHCLAF	XFXXXXXF		690
95	19	POL	529	AFPHCLAFSY	XFXXXXXXXXY		691
95	19	POL	529	AFPHCLAFSYM	XFXXXXXXXXXM		692
95	19	X	62	AFSSAGPCAL	XFXXXXXXXXL	0.0012	693
90	18	POL	535	AFSYMDDVVL	XFXXXXXXXXL	0.0009	694
95	19	POL	655	AFTFSPTY	XFXXXXXY		695
95	19	POL	655	AFTFSPTYKAF	XFXXXXXXXXXF		696
95	19	POL	521	AICSVVRRAF	XIXXXXXXF		697
90	18	NUC	58	AILCWGEL	XIXXXXXL		698
90	18	NUC	58	AILCWGELM	XIXXXXXXM		699
95	19	POL	642	ALMPLYACI	XLXXXXXXI		700
95	19	NUC	54	ALRQAILCW	XLXXXXXXW		701
80	16	ENV	108	AMQWNSTTF	XMXXXXXXF		702
95	19	POL	690	ATPTGWGL	XTXXXXXL		703
75	15	POL	690	ATPTGWGLAI	XTXXXXXXXI		704
95	19	POL	397	AVPNLQSL	XVXXXXXL		705
95	19	POL	397	AVPNLQSLTNL	XVXXXXXXXXL		706
100	20	NUC	131	AYRPPNAPI	XYXXXXXXI	0.0260	707
100	20	NUC	131	AYRPPNAPIL	XYXXXXXXXL	0.0220	708
75	15	POL	607	CFRKL PVNRPI	XFXXXXXXXXXI		709
100	20	ENV	312	CIPISSW	XIXXXXXW		710
100	20	ENV	312	CIPISSWAF	XIXXXXXXF		711
85	17	NUC	23	CLGWLWGM	XLXXXXXM		712
85	17	NUC	23	CLGWLWGM DI	XLXXXXXXXI		713
100	20	ENV	253	CLIFLLVL	XLXXXXXL		714
100	20	ENV	253	CLIFLLVLL	XLXXXXXXL		715
95	19	ENV	253	CLIFLLVLLDY	XLXXXXXXXY		716
95	19	ENV	239	CLRRFIIF	XLXXXXXF		717
95	19	ENV	239	CLRRFIIFL	XLXXXXXXL		718
75	15	ENV	239	CLRRFIIFLF	XLXXXXXXXF		719
75	15	ENV	239	CLRRFIIFLFI	XLXXXXXXXI		720
100	20	ENV	310	CTCIPSSW	XTXXXXXXW		721
90	18	NUC	31	DIDPYKEF	XIXXXXXF		722
85	17	NUC	29	DLLDTASAL	XLXXXXXXL		723
85	17	NUC	29	DLLDTASALY	XLXXXXXXXY		724
95	19	POL	40	DLNLGNLNSI	XLXXXXXXXI		725
80	16	NUC	32	DTASALYREAL	XTXXXXXXXL		726
85	17	POL	618	DWKVCQRI	XWXXXXXI		727
85	17	POL	618	DWKVCQRI VGL	XWXXXXXXXL		728
90	18	ENV	262	DYQGM LPVCPL	XYXXXXXXXL	0.0002	729
80	16	X	122	ELGEEIRL	XLXXXXXL		730
95	19	NUC	43	ELLSPLPSDF	XLXXXXXXXF		731
95	19	NUC	43	ELLSPLPSDF F	XLXXXXXXXF		732
90	18	NUC	117	EYLVSGVW	XYXXXXXXW		733
90	18	NUC	117	EYLVSGVW I	XYXXXXXXXI	0.0340	734
100	20	ENV	382	FFCLWVYI	XFXXXXXI		735
80	16	ENV	182	FLLTRIL	XFXXXXXL		736
80	16	ENV	182	FLLTRILT I	XFXXXXXXXI		737
85	17	ENV	13	FFPDHOLDPAF	XFXXXXXXXF		738
80	16	ENV	243	FIIFLFI	XIXXXXXL		739
80	16	ENV	243	FIIFLFI LL	XIXXXXXXL		740
80	16	ENV	243	FIIFLFI LL L	XIXXXXXXXL		741
80	16	ENV	248	FILLCLI	XIXXXXXI		742
80	16	ENV	248	FILLCLIF	XIXXXXXXF		743
80	16	ENV	248	FILLCLIFL	XIXXXXXXL		744
80	16	ENV	248	FILLCLIFLL	XIXXXXXXXL		745
80	16	ENV	246	FLFILLCL	XLXXXXXL		746
80	16	ENV	246	FLFILLCLI	XLXXXXXXI		747
80	16	ENV	246	FLFILLCLIF	XLXXXXXXXF		748
75	15	ENV	171	FLGPLLV	XLXXXXXL		749
95	19	POL	513	FLLAQFTSAI	XLXXXXXXXI		750
95	19	POL	562	FLLSLGIHL	XLXXXXXXL		751
80	16	ENV	183	FLLTRILT I	XLXXXXXXXI		752
95	19	ENV	256	FLLVLLDY	XLXXXXXY		753
95	19	ENV	256	FLLVLLDYQGM	XLXXXXXXXM		754
95	19	POL	656	FTFSPTYKAF	XTXXXXXXXF		755
95	19	POL	656	FTFSPTYKAF L	XTXXXXXXXL		756
95	19	POL	635	FTQCGYPAL	XTXXXXXXL		757
95	19	POL	635	FTQCGYPAL M	XTXXXXXXXM		758
95	19	ENV	346	FVGLSPTVW	XVXXXXXXW		759
95	19	ENV	346	FVGLSPTVW L	XVXXXXXXXL		760
90	18	X	132	FVLGGCRHKL	XVXXXXXXXL		761
95	19	ENV	342	FVQWVGL	XVXXXXXL		762
90	18	POL	766	FVYVPSAL	XVXXXXXL		763
95	19	POL	630	GFAAPFTQCGY	XFXXXXXXXY		764
80	16	ENV	181	GFFLLTRI	XFXXXXXI		765
80	16	ENV	181	GFFLLTRIL	XFXXXXXXL		766
80	16	ENV	181	GFFLLTRILT I	XFXXXXXXXI		767
95	19	ENV	12	GFFPDHQL	XFXXXXXL		768
75	15	ENV	170	GFLGPLLV	XFXXXXXXL		769
80	16	POL	500	GFRKIPMGVGL	XFXXXXXXXL		770
95	19	POL	627	GLLGFAAPF	XLXXXXXXF		771
95	19	POL	509	GLSPFLAQF	XLXXXXXXXF		772

Table X

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Conservancy	Freq	Protein	Position	Sequence	String	A*2401	SEQ ID NO:
100	20	ENV	348	GLSPTVWL	XLXXXXXL		773
75	15	ENV	348	GLSPTVWLSVI	XLXXXXXXXXXI		774
85	17	NUC	29	GMDIDPYKEF	XMXXXXXXXXXF		775
90	18	ENV	265	GMLPVCPL	XMXXXXXL		776
90	18	POL	735	GTDNSVL	XTXXXXXL		777
75	15	ENV	13	GTNLVSNPL	XTXXXXXXXXXL		778
80	16	POL	763	GTSFVYVPSAL	XTXXXXXXXXXL		779
80	16	POL	507	GVGLSPFL	XVXXXXXL		780
80	16	POL	507	GVGLSPFLL	XVXXXXXL		781
95	19	NUC	123	GVWIRTPPAY	XVXXXXXXXXXY		782
85	17	NUC	25	GWLVGMNDI	XWXXXXXI		783
85	17	NUC	25	GWLVGMNDIDPY	XWXXXXXXXXXY		784
85	17	ENV	65	GWSPQAQGI	XWXXXXXI	0.0024	785
85	17	ENV	65	GWSPQAQGIIL	XWXXXXXXXXXL	0.0003	786
95	19	POL	639	GYPALMPL	XYXXXXXL		787
95	19	POL	639	GYPALMPLY	XYXXXXXXXXXY	0.0490	788
95	19	ENV	234	GYRWMCLRRF	XYXXXXXXXXXF	0.0110	789
95	19	ENV	234	GYRWMCLRRFI	XYXXXXXXXXXI		790
85	17	POL	579	GYSLNFMGY	XYXXXXXXXXXY	0.0002	791
75	15	POL	579	GYSLNFMGYVI	XYXXXXXXXXXI		792
80	16	POL	820	HFASPLHVAW	XFXXXXXXXXW		793
75	15	POL	7	HFRKLLL	XFXXXXXL		794
80	16	POL	435	HLLVGSSGL	XLXXXXXL		795
75	15	POL	569	HLNPNKTKRW	XLXXXXXXXXW		796
80	16	POL	491	HLYSHPII	XLXXXXXI		797
80	16	POL	491	HLYSHPIIL	XLXXXXXL		798
80	16	POL	491	HLYSHPIILGF	XLXXXXXXXXXF		799
85	17	POL	715	HTAELLAACF	XTXXXXXXXXXF		800
100	20	NUC	52	HTALRQAI	XTXXXXXI		801
95	19	NUC	52	HTALRQAIL	XTXXXXXL		802
95	19	NUC	52	HTALRQAILCW	XTXXXXXXXXXW		803
100	20	POL	149	HTLWKAGI	XTXXXXXI		804
100	20	POL	149	HTLWKAGIL	XTXXXXXL		805
100	20	POL	149	HTLWKAGILY	XTXXXXXXXXXY		806
100	20	POL	146	HYLHTLWKAGI	XYXXXXXXXXXI		807
100	20	ENV	381	IFFCLWVY	XFXXXXXY		808
100	20	ENV	381	IFFCLWVYI	XFXXXXXI	0.0087	809
80	16	ENV	245	IFLFILL	XFXXXXXL		810
80	16	ENV	245	IFLFILLCL	XFXXXXXXXXXL		811
80	16	ENV	245	IFLFILLCLI	XFXXXXXXXXXI		812
95	19	ENV	255	IFLVLLDY	XFXXXXXY		813
80	16	ENV	244	IIFLFI	XIXXXXXL		814
80	16	ENV	244	IIFLFI	XIXXXXXL		815
80	16	ENV	244	IIFLFI	XIXXXXXL		816
80	16	ENV	244	IIFLFI	XIXXXXXL		817
80	16	POL	497	IILGFRKI	XIXXXXXXI		818
80	16	POL	497	IILGFRKIPM	XIXXXXXXMX		819
90	18	NUC	59	ILCWGELM	XLXXXXXM		820
80	16	POL	498	ILGFRKIPM	XLXXXXXMX		821
100	20	ENV	249	ILLCLIF	XLXXXXXF		822
100	20	ENV	249	ILLCLIFL	XLXXXXXL		823
100	20	ENV	249	ILLCLIFLL	XLXXXXXMX		824
80	16	POL	760	ILRGTSFVY	XLXXXXXY		825
95	19	ENV	188	ILTIQSL	XLXXXXXL		826
90	18	ENV	188	ILTIQSLDSW	XLXXXXXXXXXW		827
90	18	POL	625	IVGLLGFAAPF	XVXXXXXXXXXF		828
85	17	ENV	358	IWMWVYWGSPS	XWXXXXXXXXXL	0.0004	829
95	19	POL	395	KFAVPNLQSL	XFXXXXXXXXXL	0.0020	830
80	16	POL	503	KIPMGVGL	XIXXXXXL		831
80	16	POL	503	KIPMGVGLSPF	XIXXXXXXXXXF		832
85	17	NUC	21	KLCGLWLW	XLXXXXW		833
85	17	NUC	21	KLCGLWLWGM	XLXXXXXXXXMX		834
95	19	POL	489	KLHLYSHPI	XLXXXXXI		835
80	16	POL	489	KLHLYSHPII	XLXXXXXMX		836
80	16	POL	489	KLHLYSHPIIL	XLXXXXXXXXXL		837
75	15	POL	108	KLIMPARF	XLXXXXXF		838
75	15	POL	108	KLIMPARFY	XLXXXXXY		839
80	16	POL	610	KLPVNRPI	XLXXXXXI		840
80	16	POL	610	KLPVNRPIDW	XLXXXXXXXXXW		841
95	19	POL	574	KTKRWGYSL	XTXXXXXL		842
85	17	POL	574	KTKRWGYSLNF	XTXXXXXXXXXF		843
85	17	POL	620	KVCORIVGL	XVXXXXXL		844
85	17	POL	620	KVCORIVGLL	XVXXXXXXXXXL		845
95	19	POL	55	KVGNFTGL	XVXXXXXL		846
95	19	POL	55	KVGNFTGLY	XVXXXXXY		847
85	17	X	91	KVLHKRTL	XVXXXXXL		848
85	17	X	91	KVLHKRTLGL	XVXXXXXXXXXL		849
100	20	POL	121	KYLPDKGI	XYXXXXXI	0.0028	850
85	17	POL	745	KYTSFPWL	XYXXXXXL		851
85	17	POL	745	KYTSFPWLL	XYXXXXXL	3.6000	852
80	16	ENV	247	LFILLCL	XFXXXXXL		853
80	16	ENV	247	LFILLCLI	XFXXXXXI		854
80	16	ENV	247	LFILLCLIF	XFXXXXXXXXF		855
80	16	ENV	247	LFILLCLIFL	XFXXXXXXXXXL		856

Table X

HBV A24 SUPER MOTIF (With binding information)

Conservancy	Freq	Protein	Position	Sequence	String	A*2401	SEQ ID NO:
100	20	EN	254	LIFLLVLL	XIXXXXXXL		856
95	19	EN	254	LIFLLVLLDY	XIXXXXXXXY		857
100	20	POL	109	LIMPARFY	XIXXXXXY		858
95	19	POL	514	LLAQFTSAI	XLXXXXXXI		859
100	20	EN	251	LLCLIFLL	XLXXXXXL		860
100	20	EN	251	LLCLIFLLVL	XLXXXXXXXL		861
100	20	EN	251	LLCLIFLLVLL	XLXXXXXXXL		862
85	17	NUC	30	LLDTASAL	XLXXXXXL		863
85	17	NUC	30	LLDTASALY	XLXXXXXXY		864
95	19	EN	260	LLDYOGML	XLXXXXXL		865
80	16	POL	752	LLGCAANW	XLXXXXXW		866
80	16	POL	752	LLGCAANWI	XLXXXXXXI		867
80	16	POL	752	LLGCAANWIL	XLXXXXXXXL		868
95	19	POL	628	LLGFAAPF	XLXXXXXF		869
75	15	EN	63	LLGWSPOAQGI	XLXXXXXXXI		870
100	20	EN	250	LLLCLIFL	XLXXXXXL		871
100	20	EN	250	LLLCLIFLL	XLXXXXXL		872
100	20	EN	250	LLLCLIFLLVL	XLXXXXXXXL		873
100	20	EN	378	LLPIFFCL	XLXXXXXL		874
100	20	EN	378	LLPIFFCLW	XLXXXXXW		875
100	20	EN	378	LLPIFFCLWVY	XLXXXXXXY		876
95	19	NUC	44	LLSFLPSDF	XLXXXXXF		877
95	19	NUC	44	LLSFLPSDF	XLXXXXXXF		878
95	19	POL	563	LLSLGIHL	XLXXXXXL		879
90	18	POL	407	LLSSNLWS	XLXXXXXW		880
90	18	POL	407	LLSSNLWSL	XLXXXXXXL		881
90	18	POL	407	LLSSNLWSLSL	XLXXXXXXXL		882
80	16	EN	184	LLTRILT	XLXXXXXI		883
80	16	POL	436	LLVGSSGL	XLXXXXXL		884
95	19	EN	257	LLVLLDYOGM	XLXXXXXXM		885
95	19	EN	257	LLVLLDYOGML	XLXXXXXXXL		886
95	19	EN	175	LLVLQAGF	XLXXXXXF		887
95	19	EN	175	LLVLQAGFF	XLXXXXXXF		888
90	18	EN	175	LLVLQAGFFL	XLXXXXXXXL		889
90	18	EN	175	LLVLQAGFFLL	XLXXXXXXXL		890
100	20	EN	338	LLVPFVQW	XLXXXXXW		891
100	20	EN	338	LLVPFVQWF	XLXXXXXXF		892
90	18	NUC	100	LLWFHISCL	XLXXXXXL		893
85	17	NUC	100	LLWFHISCLTF	XLXXXXXXF		894
95	19	POL	643	LMPLYACI	XMXXXXXI		895
75	15	NUC	137	LTFGRETVL	XTXXXXXXL		896
75	15	NUC	137	LTFGRETVLEY	XTXXXXXXY		897
90	18	EN	189	LTIQSLDSW	XTXXXXXXW		898
90	18	EN	189	LTIQSLDSWW	XTXXXXXXW		899
90	18	POL	404	LTNLLSSNL	XTXXXXXXL		900
90	18	POL	404	LTNLLSSNLWS	XTXXXXXXW		901
80	16	EN	185	LTRILTIPQSL	XTXXXXXXXL		902
85	17	POL	99	LTVNEKRRL	XTXXXXXXL		903
95	19	EN	258	LVLLDYOGM	XVXXXXXXM		904
95	19	EN	258	LVLLDYOGML	XVXXXXXXXL		905
95	19	EN	176	LVLOAGFF	XVXXXXXF		906
90	18	EN	176	LVLOAGFFL	XVXXXXXXL		907
90	18	EN	176	LVLOAGFFLL	XVXXXXXXXL		908
100	20	EN	339	LVPFVQWF	XVXXXXXF		909
95	19	EN	339	LVPFVQWVGL	XVXXXXXXXL		910
90	18	NUC	119	LVSFGVWI	XVXXXXXI		911
100	20	POL	377	LVVDFSQF	XVXXXXXF		912
90	18	NUC	101	LWFHISCL	XWXXXXXL		913
85	17	NUC	101	LWFHISCLTF	XWXXXXXXF		914
85	17	NUC	27	LWGMDIDPY	XWXXXXXY		915
100	20	POL	151	LWKAGILY	XWXXXXXY		916
80	16	POL	492	LYSHPIIL	XYXXXXXL		917
80	16	POL	492	LYSHPIILGF	XYXXXXXXF	1.1000	918
85	17	EN	360	MMWYWGPSL	XMXXXXXL	0.0012	919
85	17	EN	360	MMWYWGPSLY	XMXXXXXXY	0.0001	920
85	17	EN	361	MWYWGPSL	XWXXXXXL		921
85	17	EN	361	MWYWGPSLY	XWXXXXXY	0.0027	922
95	19	POL	561	NFLSLGI	XFXXXXXI		923
95	19	POL	561	NFLSLGIHL	XFXXXXXXL	0.0099	924
95	19	POL	42	NLGNLNSI	XLXXXXXI		925
95	19	POL	42	NLGNLNSIPW	XLXXXXXXW		926
90	18	POL	406	NLLSSNLWS	XLXXXXXW		927
90	18	POL	406	NLLSSNLWSL	XLXXXXXXL		928
95	19	POL	45	NLNSIPW	XLXXXXXW		929
100	20	POL	400	NLOSLTNL	XLXXXXXL		930
100	20	POL	400	NLOSLTNLL	XLXXXXXL		931
75	15	EN	15	NLSVNPPL	XLXXXXXL		932
75	15	EN	15	NLSVNPPLGF	XLXXXXXXF		933
80	16	POL	758	NWILRGTSF	XWXXXXXF		934
80	16	POL	758	NWILRGTSFVY	XWXXXXXXY		935
95	19	POL	512	PFLLAQFTSAI	XFXXXXXXI		936
95	19	POL	634	PFTQCGYPAL	XFXXXXXXL	0.0002	937
95	19	POL	634	PFTQCGYPALM	XFXXXXXXM		938

Table X

HBV A24 SUPER MOTIF (With binding information)

Conservancy	Freq	Protein	Position	Sequence	String	A*2401	SEQ ID NO:
95	19	ENW	341	PFVOWFVGL	XFXXXXXXL	0.0003	939
85	17	POL	616	PIDWKVQRI	XIXXXXXXXI		940
100	20	ENW	380	PIFFCLWVY	XIXXXXXXY		941
100	20	ENW	380	PIFFCLWVYI	XIXXXXXXXI		942
85	17	POL	713	PIHTAELL	XIXXXXXL		943
80	16	POL	496	PIILGFRKI	XIXXXXXXI		944
80	16	POL	496	PIILGFRKIPM	XIXXXXXXXM		945
100	20	ENW	314	PIPSSWAF	XIXXXXXF		946
100	20	POL	124	PLDKGIKPY	XLXXXXXXY		947
100	20	POL	124	PLDKGIKPYY	XLXXXXXXY		948
95	19	POL	20	PLEELPRL	XLXXXXXXL		949
95	19	ENW	10	PLGFFPDHQL	XLXXXXXXL		950
100	20	POL	427	PLHPAAMPHL	XLXXXXXXL		951
100	20	POL	427	PLHPAAMPHLL	XLXXXXXXL		952
100	20	ENW	377	PLLPIFFCL	XLXXXXXXL		953
100	20	ENW	377	PLLPIFFCLW	XLXXXXXXW		954
95	19	ENW	174	PLLVLQAGF	XLXXXXXXF		955
95	19	ENW	174	PLLVLQAGFF	XLXXXXXXF		956
90	18	ENW	174	PLLVLQAGFLL	XLXXXXXXL		957
80	16	POL	711	PLPIHTAEL	XLXXXXXXL		958
80	16	POL	711	PLPIHTAELL	XLXXXXXXL		959
75	15	POL	2	PLSYQHFRKL	XLXXXXXXL		960
75	15	POL	2	PLSYQHFRKLL	XLXXXXXXL		961
85	17	POL	98	PLTVNEKRRL	XLXXXXXXL		962
80	16	POL	505	PMGVGLSPF	XMXXXXXXF		963
80	16	POL	505	PMGVGLSPFL	XMXXXXXXL		964
80	16	POL	505	PMGVGLSPFLL	XMXXXXXXL		965
75	15	POL	692	PTGWGLAI	XTXXXXXI		966
85	17	POL	797	PTTGRTSL	XTXXXXXL		967
85	17	POL	797	PTTGRTSLY	XTXXXXXXY		968
80	16	NUC	15	PTVQASKL	XTXXXXXL		969
80	16	NUC	15	PTVQASKLCL	XTXXXXXXL		970
75	15	ENW	351	PTVWLSVI	XTXXXXXI		971
75	15	ENW	351	PTVWLSVIW	XTXXXXXXW		972
75	15	ENW	351	PTVWLSVIWM	XTXXXXXXM		973
85	17	POL	612	PVNRPIDW	XVXXXXXXW		974
80	16	POL	750	PWLLGCAANW	XWXXXXXXW		975
80	16	POL	750	PWLLGCAANWI	XWXXXXXXI		976
100	20	POL	51	PWTHKVGNF	XWXXXXXXF	0.0290	977
80	16	X	8	QLDPARDVL	XLXXXXXXL		978
80	16	X	8	QLDPARDVLCL	XLXXXXXXL		979
90	18	NUC	99	QLLWFHISCL	XLXXXXXXL		980
95	19	POL	685	QVFADATPTGW	XVXXXXXXW		981
95	19	ENW	344	QWVFGLSPTVW	XWXXXXXXW		982
75	15	ENW	242	RFIIFLFI	XFXXXXXI		983
75	15	ENW	242	RFIIFLFIL	XFXXXXXXL		984
75	15	ENW	242	RFIIFLFIIL	XFXXXXXXL		985
75	15	ENW	242	RFIIFLFIILL	XFXXXXXXL		986
100	20	ENW	332	RFSWLSLL	XFXXXXXL		987
100	20	ENW	332	RFSWLSLLVPF	XFXXXXXXF		988
80	16	ENW	187	RILTIQSL	XIXXXXXL		989
90	18	POL	624	RIVGLLG	XIXXXXXF		990
75	15	POL	106	RLKLIMPARF	XLXXXXXXF		991
75	15	POL	106	RLKLIMPARFY	XLXXXXXXY		992
95	19	POL	376	RLVVDFSQF	XLXXXXXXF		993
90	18	POL	353	RTPARVTGGVF	XTXXXXXXF		994
95	19	POL	36	RVAEDNLN	XVXXXXXL		995
90	18	POL	36	RVAEDNLNLN	XVXXXXXXL		996
80	16	POL	818	RVHFASPL	XVXXXXXL		997
100	20	POL	357	RVTGGVRL	XVXXXXXL		998
85	17	POL	577	RWGYSUNF	XWXXXXXXF		999
85	17	POL	577	RWGYSUNFM	XWXXXXXXM		1000
85	17	POL	577	RWGYSUNFMGY	XWXXXXXXY		1001
95	19	ENW	236	RWMCLRRF	XWXXXXXF		1002
95	19	ENW	236	RWMCLRRFI	XWXXXXXXI	0.0710	1003
95	19	ENW	236	RWMCLRRFII	XWXXXXXXI	1.1000	1004
95	19	ENW	236	RWMCLRRFIIF	XWXXXXXXF		1005
100	20	POL	167	SFCGSPYSW	XFXXXXXXW	0.0710	1006
95	19	NUC	46	SFLPSDF	XFXXXXXF		1007
80	16	POL	765	SFVYVPSAL	XFXXXXXXL		1008
100	20	POL	49	SIPWTHKVGNF	XIXXXXXXXF		1009
95	19	ENW	194	SLDSWWTSL	XLXXXXXXL		1010
95	19	ENW	194	SLDSWWTSLNF	XLXXXXXXF		1011
95	19	POL	416	SLDVSAAF	XLXXXXXF		1012
95	19	POL	416	SLDVSAAFY	XLXXXXXXY		1013
100	20	ENW	337	SLLVPFVQW	XLXXXXXXW		1014
100	20	ENW	337	SLLVPFVQWF	XLXXXXXXF		1015
75	15	POL	581	SLNFMGYVI	XLXXXXXXI		1016
95	19	X	54	SLRGLPVCAF	XLXXXXXXF		1017
90	18	POL	403	SLTNLLSSNL	XLXXXXXXL		1018
75	15	X	104	STTDLEAY	XTXXXXXXY		1019
75	15	X	104	STTDLEAYF	XTXXXXXXF		1020
75	15	ENW	17	SVPNPLGF	XVXXXXXF		1021

Table X

HBV A24 SUPER MOTIF (With binding information)

Conservancy	Freq	Protein	Position	Sequence	String	A*2401	SEQ ID NO:
85	17	POL	548	SVQHLESL	XVXXXXXL		1022
80	16	ENV	330	SVRFWSLSL	XVXXXXXXL		1023
80	16	ENV	330	SVRFWSLSLL	XVXXXXXXXL		1024
90	18	POL	739	SVVLSRKY	XVXXXXXY		1025
85	17	POL	739	SVVLSRKYTSF	XVXXXXXXXFX		1026
95	19	POL	524	SVVRRAFPCL	XVXXXXXXXL		1027
95	19	POL	413	SWLSLDVSAAF	XWXXXXXXXFX		1028
100	20	ENV	334	SWLSLLVPF	XWXXXXXXXFX	0.3900	1029
95	19	POL	392	SWPKFAVPNL	XWXXXXXXXL	5.6000	1030
100	20	ENV	197	SWWTSLSNF	XWXXXXXXXFX		1031
95	19	ENV	197	SWWTSLSNLF	XWXXXXXXXL	0.3800	1032
90	18	POL	537	SYMDDVVL	XYXXXXXL		1033
75	15	POL	4	SYQHFRKL	XYXXXXXL		1034
75	15	POL	4	SYQHFRKLL	XYXXXXXXL	0.0051	1035
75	15	POL	4	SYQHFRKLLL	XYXXXXXXXL	0.0660	1036
75	15	POL	4	SYQHFRKLLLL	XYXXXXXXXXL		1037
75	15	NUC	138	TFGRETVL	XFXXXXXL		1038
75	15	NUC	138	TFGRETVLEY	XFXXXXXXXXY		1039
75	15	NUC	138	TFGRETVLEYL	XFXXXXXXXXL		1040
95	19	POL	657	TFSPITYKAF	XFXXXXXXXFX	0.0060	1041
95	19	POL	657	TFSPITYKAF	XFXXXXXXXXL	0.0043	1042
90	18	ENV	190	TIPQSLDSW	XIXXXXXXW		1043
90	18	ENV	190	TIPQSLDSWW	XIXXXXXXXXW		1044
100	20	POL	150	TLWKAGIL	XLXXXXXL		1045
100	20	POL	150	TLWKAGILY	XLXXXXXXY		1046
75	15	X	105	TTDLEAYF	XTXXXXFX		1047
85	17	POL	798	TTGRTSLY	XTXXXXXY		1048
85	17	POL	100	TVNEKRR	XVXXXXXL		1049
80	16	NUC	16	TVQASKLCL	XVXXXXXXL		1050
80	16	NUC	16	TVQASKLCLGW	XVXXXXXXXW		1051
75	15	ENV	352	TVWLSVIW	XVXXXXXW		1052
75	15	ENV	352	TVWLSVIWM	XVXXXXXXM		1053
95	19	POL	686	VFADATPTGW	XFXXXXXXXW	0.0180	1054
75	15	X	131	VFLGGCRHKL	XFXXXXXXXL		1055
85	17	POL	543	VLGAKSVQHL	XLXXXXXXL		1056
90	18	X	133	VLGGCRHKL	XLXXXXXXL		1057
85	17	X	92	VLHKRTLGL	XLXXXXXXL		1058
95	19	ENV	259	VLLDYQGM	XLXXXXXM		1059
95	19	ENV	259	VLLDYQGML	XLXXXXXXL		1060
95	19	ENV	177	VLOAGFFL	XLXXXXXL		1061
95	19	ENV	177	VLOAGFFLL	XLXXXXXXL		1062
85	17	POL	741	VLSRKYTSF	XLXXXXXXXFX		1063
85	17	POL	741	VLSRKYTSFPW	XLXXXXXXXW		1064
80	16	POL	542	VVLGAKSVQHL	XVXXXXXXXL		1065
85	17	POL	740	VVLSRKYTSF	XVXXXXXXXFX		1066
95	19	POL	525	VVRRAFPCL	XVXXXXXXXL		1067
95	19	NUC	124	VWIRTPPAY	XWXXXXXXY		1068
75	15	ENV	353	VWLSVIWM	XWXXXXXM		1069
90	18	NUC	102	WFHISCLTF	XFXXXXXXXFX	0.0300	1070
95	19	ENV	345	WFGVLSPTVW	XFXXXXXXXW	0.0120	1071
95	19	ENV	345	WFGVLSPTVWL	XFXXXXXXXXL		1072
80	16	POL	759	WILRGTSF	XIXXXXXFX		1073
80	16	POL	759	WILRGTSFVY	XIXXXXXXXY		1074
95	19	NUC	125	WIRTPPAY	XIXXXXXY		1075
80	16	POL	751	WLLGCAANW	XLXXXXXXW		1076
80	16	POL	751	WLLGCAANWI	XLXXXXXXI		1077
80	16	POL	751	WLLGCAANWIL	XLXXXXXXXL		1078
95	19	POL	414	WLSLDVSAAF	XLXXXXXXXFX		1079
95	19	POL	414	WLSLDVSAAFY	XLXXXXXXXXY		1080
100	20	ENV	335	WLSLLVPF	XLXXXXFX		1081
100	20	ENV	335	WLSLLVPFVQW	XLXXXXXXXW		1082
85	17	NUC	26	WLWGMDIDPY	XLXXXXXXY		1083
95	19	ENV	237	WMCLRRFI	XMXXXXXI		1084
95	19	ENV	237	WMCLRRFII	XMXXXXXXI	0.0230	1085
95	19	ENV	237	WMCLRRFIIF	XMXXXXXXXFX	0.0013	1086
95	19	ENV	237	WMCLRRFIIFL	XMXXXXXXXL		1087
85	17	ENV	359	WMMWYWGPSL	XMXXXXXXXL	0.0005	1088
85	17	ENV	359	WMMWYWGPSL	XMXXXXXXXXY		1089
100	20	POL	52	WTHKVGNF	XTXXXXFX		1090
95	19	POL	52	WTHKVGNFGL	XTXXXXXXXL		1091
95	19	ENV	198	WWTSLSNLF	XWXXXXXL		1092
85	17	ENV	362	WYWGPSLY	XYXXXXXY	0.0001	1093
100	20	POL	147	YLHTLWKAGI	XLXXXXXXI		1094
100	20	POL	147	YLHTLWKAGIL	XLXXXXXXXL		1095
100	20	POL	122	YLPDKGI	XLXXXXXI		1096
100	20	POL	122	YLPDKGIKPY	XLXXXXXXXXY		1097
90	18	NUC	118	YLVSGVW	XLXXXXXW		1098
90	18	NUC	118	YLVSGVWI	XLXXXXXI		1099
85	17	POL	746	YTSFPWLL	XTXXXXXL		1100

HBV B07 SUPER MOTIF (With binding information)

Table XI

Conservancy	Frequency	Protein	Position	Sequence	P2	C-term	AA	B*0702	B*3501	B*5101	B*5301	B*5401	SEQIDNO
75	15	X	146	APCNFTSA	P	A	9						1101
95	19	POL	633	APFTOCGY	P	Y	8						1102
95	19	POL	633	APFTOCGYPA	P	A	10						1103
95	19	POL	633	APFTOCGYPAL	P	L	11						1104
100	20	BW	232	CPGYRMQL	P	L	9						1105
80	16	NJC	14	CPTVQASKL	P	L	9						1106
80	16	NJC	14	CPTVQASKLCL	P	L	11						1107
80	16	X	10	DPAVDLCL	P	L	9						1108
80	16	BW	122	DPRVRGLY	P	Y	8						1109
90	18	POL	778	DPSRGLGL	P	L	9						1110
90	18	NJC	33	DPYKEFGA	P	A	8						1111
75	15	BW	130	FPAGSSSGTV	P	V	11						1112
90	18	BW	14	FPDHOLDPA	P	A	9						1113
85	17	BW	14	FPDHOLDPAF	P	F	10						1114
95	19	POL	530	FPHCLAFSY	P	Y	9						1115
95	19	POL	530	FPHCLAFSYM	P	M	10						1116
75	15	POL	749	FPWLLGCA	P	A	8						1117
75	15	POL	749	FPWLLGCAA	P	A	9						1118
75	15	POL	749	FPWLLGCAANW	P	W	11						1119
90	18	X	67	GPCALFTSA	P	A	10						1120
95	19	POL	19	GPLEEBPRL	P	L	10						1121
90	18	POL	19	GPLEEBPRLA	P	A	11						1122
95	19	BW	173	GPLLVLQA	P	A	8						1123
95	19	BW	173	GPLLVLQAGF	P	F	10						1124
95	19	BW	173	GPLLVLQAGFF	P	F	11						1125
85	17	POL	97	GPLTVNEKRRL	P	L	11						1126
100	20	POL	429	HPAAMPHL	P	L	8						1127
100	20	POL	429	HPAAMPHLL	P	L	9						1128
85	17	POL	429	HPAAMPHLLV	P	V	10						1129
80	16	POL	495	HPILLGFRKI	P	I	10						1130
100	20	BW	313	IPISSWA	P	A	8						1131
100	20	BW	313	IPISSWAF	P	F	9						1132
80	16	BW	313	IPISSWAF	P	A	10						1133
80	16	POL	504	IPMGVGLSPF	P	F	10						1134
80	16	POL	504	IPMGVGLSPFL	P	L	11						1135
90	18	BW	191	IPOSLSW	P	W	8						1136
90	18	BW	191	IPOSLSWW	P	W	9						1137
80	16	BW	315	IPSSWAF	P	A	8						1138
100	20	POL	50	IPWTHKVGNF	P	F	10						1139
100	20	BW	379	LPIFFCLW	P	W	8						1140
100	20	BW	379	LPIFFCLWY	P	Y	9						1141
100	20	BW	379	LPIFFCLWYI	P	I	11						1142
100	20	BW	379	LPIFFCLWYI	P	I	11						1143
85	17	POL	712	LPIHTAEL	P	L	8						1144
85	17	POL	712	LPIHTAEL	P	L	9						1145
85	17	POL	712	LPIHTAELLA	P	A	10						1146
85	17	POL	712	LPIHTAELLA	P	A	11						1147
80	16	X	89	LPKVLHKRTL	P	L	10						1148

HBV B07 SUPER MOTIF (With binding information)

Table XI

Conservancy	Frequency	Protein	Position	Sequence	P2	C-term	AA	B*0702	B*3501	B*5101	B*5301	B*5401	SEQ ID NO
100	20	POL	123	LPLDKGIKPY	P	Y	10	0.0001	0.0290	0.0002	0.0003	0.0002	1149
100	20	POL	123	LPLDKGIKPY	P	Y	11	-0.0002	0.0009	0.0001	0.0007	0.0001	1150
95	19	X	58	LPVCAFFSA	P	A	9	0.0480	0.0710	0.0110	0.0009	19.0000	1151
80	16	POL	611	LPVNRPIDW	P	W	9						1152
80	16	POL	611	LPVNRPIDWKV	P	V	11						1153
80	16	POL	433	MPHLVGSSGL	P	L	11						1154
100	20	POL	1	MPLSYQH	P	F	8	0.0001	0.0097	0.0120	0.0370	0.0190	1155
75	15	POL	1	MPLSYQHFRKL	P	L	11						1156
90	18	POL	774	NPADOPSRGRL	P	L	11	0.0120	0.0001	0.0001	-0.0003	0.0001	1157
95	19	EW	9	NPLGFFPDHQL	P	L	11	0.0012	0.0021	0.0001	0.0028	0.0001	1158
75	15	POL	571	NPNTKRW	P	W	8						1159
75	15	POL	571	NPNTKRWGY	P	Y	10						1160
95	19	NJC	129	PPAYRPPNA	P	A	9	0.0001	0.0001	0.0001	0.0002	0.0003	1161
95	19	NJC	129	PPAYRPPNAPI	P	I	11	0.0003	0.0001	0.0001	-0.0003	0.0001	1162
85	17	EW	58	PPHGGILGW	P	W	9	0.0001	0.0002	0.0001	0.0003	0.0002	1163
100	20	NJC	134	PPNAPILSTL	P	L	10	0.0001	0.0001	0.0035	0.0001	0.0002	1164
80	16	POL	615	RPIDWKVCORI	P	I	11						1165
100	20	NJC	133	RPPNAPIL	P	L	8	0.0076	0.0001	0.0280	0.0002	0.0002	1166
100	20	NJC	133	RPPNAPILSTL	P	L	11	0.1300	0.0001	0.0018	-0.0003	0.0001	1167
100	20	NJC	44	SPEHCSPHHTA	P	A	11	-0.0002	0.0001	0.0001	-0.0003	0.0011	1168
95	19	POL	511	SPFLAOF	P	F	8	0.5500	0.0009	0.0180	0.0009	0.0093	1169
95	19	POL	511	SPFLAOFSTA	P	A	11	0.0820	0.0001	0.0001	-0.0003	12.0500	1170
100	20	NJC	49	SPHHTALRQA	P	A	10	0.0012	0.0001	0.0001	0.0002	0.0035	1171
100	20	NJC	49	SPHHTALRQAI	P	I	11	0.5800	0.0001	0.0004	0.0005	0.0002	1172
85	17	EW	67	SPOAQIL	P	L	8						1173
85	17	POL	808	SPSVPSHL	P	L	8						1174
75	15	EW	350	SPTVWLSV	P	V	8						1175
75	15	EW	350	SPTVWLSVI	P	I	9						1176
75	15	EW	350	SPTVWLSVW	P	W	10						1177
75	15	EW	350	SPTVWLSVWM	P	M	11						1178
95	19	POL	659	SPTYKAF	P	L	8	0.3900	0.0001	0.0019	0.0002	0.0002	1179
90	18	POL	354	TPARVTGGV	P	V	9	0.0078	0.0001	0.0013	0.0001	0.0015	1180
90	18	POL	354	TPARVTGGVF	P	F	10	0.3200	0.1000	0.0001	0.0099	0.0006	1181
90	18	POL	354	TPARVTGGVFL	P	L	11	0.0950	0.0001	0.0001	0.0005	0.0005	1182
95	19	NJC	128	TPPAYRPPNA	P	A	10	0.0001	0.0001		0.0002	0.0100	1183
75	15	EW	57	TPPHGGL	P	L	8						1184
75	15	EW	57	TPPHGGLGW	P	W	10						1185
80	16	POL	691	TPTGWGLA	P	A	8						1186
75	15	POL	691	TPTGWGLAI	P	I	9						1187
95	19	EW	340	VPPVQWVFL	P	V	8	0.0010	0.0001	19.0000	0.0002	0.1100	1188
95	19	EW	340	VPPVQWVFL	P	L	10	0.0011	0.0001	0.0100	0.0001	0.0025	1189
95	19	POL	398	VPNLQSLTNL	P	L	10	0.0006	0.0001	0.0004	0.0001	0.0002	1190
95	19	POL	398	VPNLQSLTNL	P	L	11	0.0004	0.0001	0.0001	-0.0003	0.0002	1191
90	18	POL	769	VPSALNPA	P	A	8	0.0011	0.0001	0.0070	0.0002	1.0000	1192
95	19	POL	393	WPKFAVNL	P	L	9	0.0054	0.0002	0.0015	0.0001	0.0015	1193
95	19	POL	640	YPALMPLY	P	Y	8	0.0004	0.2600	0.4100	0.0450	0.0056	1194
95	19	POL	640	YPALMPLYA	P	A	9	0.0180	0.0480	0.0340	0.0140	16.0000	1195
95	19	POL	640	YPALMPLYACI	P	I	11	0.0040	0.0001	0.0470	0.0320	0.0700	1196

HBV B27 Super Motif (No binding data available)

TABLE XII

Protein	Sequence	Position in HBV	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SeqID Num
AYW	AHLSRLGL	51	8	19	95	1197
AYW	ARVTGGVF	356	8	18	90	1198
AYW	DHGAHSL	48	8	19	95	1199
AYW	DHOLDPAF	16	8	18	90	1200
AYW	DKGIKPY	126	8	20	100	1201
AYW	FHSCLTF	103	8	18	90	1202
AYW	FRKIPMGV	501	8	16	80	1203
AYW	GRETVEY	140	8	15	75	1204
AYW	HHTALROA	51	8	20	100	1205
AYW	IHTAELLA	714	8	17	85	1206
AYW	LHKRTLGL	93	8	18	90	1207
AYW	LHLYSHPI	490	8	19	95	1208
AYW	LRGLPVCA	55	8	19	95	1209
AYW	LRGTSFVY	761	8	16	80	1210
AYW	LROAILCW	55	8	19	95	1211
AYW	LRRFIIFL	240	8	19	95	1212
AYW	NKTKRWGY	573	8	15	75	1213
AYW	NRPIDMKV	614	8	18	90	1214
AYW	NRVAEDL	34	8	17	85	1215
AYW	PHCLAFSY	531	8	19	95	1216
AYW	PHGGLGW	59	8	17	85	1217
AYW	PKFAVPNL	394	8	19	95	1218
AYW	QHFRKLL	6	8	15	75	1219
AYR	RHYLHTLW	145	8	20	100	1220
AYW	RKYTSFPW	744	8	17	85	1221
AYW	RRAPPHQL	527	8	19	95	1222
AYW	RRFIIFL	241	8	15	75	1223
AYW	SHPIILGF	494	8	16	80	1224
AYW	SKCLGWL	20	8	18	90	1225
AYW	SRNLVSL	472	8	16	80	1226
AYW	TKRWGYSL	575	8	19	95	1227
AYW	TRHYLHTL	144	8	20	100	1228
AYW	VRFWSLSL	331	8	16	80	1229
AYW	WKVQORIV	619	8	17	85	1230
AYW	YRPPNAPI	132	8	20	100	1231
AYW	ARVTGGVFL	356	9	18	90	1232
AYW	EHCSPIHITA	46	9	20	100	1233
AYW	GRETVEYL	140	9	15	75	1234
AYR	HHTALROAI	51	9	20	100	1235
AYW	HKGNFTGL	54	9	19	95	1236
AYW	IHTAELLA	714	9	17	85	1237
AYW	KRWGYSNIF	576	9	17	85	1238
AYW	LHLYSHPII	490	9	16	80	1239
AYW	LHPAAMPHL	428	9	20	100	1240
AYW	LHTLWKAGI	148	9	20	100	1241
						1242

TABLE XII
HBV B27 Super Motif (No binding data available)

Protein	Sequence	Position in HBV	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SeqID Num
AYR	LKLMPARF	107	9	15	75	1243
AYW	LRGLPVCAF	55	9	19	95	1244
AYW	LRGTSFVV	761	9	16	80	1245
AYW	LRRFIILF	240	9	15	75	1246
AYW	PHCLAFSYM	531	9	19	95	1247
AYW	PHHTALROA	50	9	20	100	1248
AYW	PKVLHKRTL	90	9	17	85	1249
AYW	QHFRKLLL	6	9	15	75	1250
AYW	QRVGLIGF	623	9	18	90	1251
AYW	RKIPMGVGL	502	9	16	80	1252
AYW	RKLPVNRPI	609	9	16	80	1253
AYW	RKYTSFPWL	744	9	17	85	1254
AYW	RRAFPCLA	527	9	19	95	1255
AYW	RRFIIIFI	241	9	15	75	1256
AYR	RRKLIMPA	105	9	15	75	1257
AYW	RRVAEDNL	35	9	18	90	1258
AYW	SKCLGLMW	20	9	17	85	1259
AYW	SRKYTSFPW	743	9	17	85	1260
AYW	TRHYLHTLW	144	9	20	100	1261
AYW	VHFASPLHV	819	9	16	80	1262
AYW	VRFWSLL	331	9	16	80	1263
AYW	VRAFPHCL	526	9	19	95	1264
AYW	YRPPNAPIL	132	9	20	100	1265
AYW	YRWMCJRRF	235	9	19	95	1266
AYW	AHLSLRGLPV	51	10	18	90	1267
AYW	AKSVOHLESL	546	10	17	85	1268
AYW	ARDVLCRPV	12	10	15	75	1269
AYW	ARVTGGVFLV	356	10	18	90	1270
AYW	EHCSPHITAL	46	10	20	100	1271
AYW	FRKIPMGVGL	501	10	16	80	1272
AYW	FRKLPVNRPI	608	10	16	80	1273
AYR	GRTVLEVLV	140	10	15	75	1274
AYW	HHTALROAIL	51	10	19	95	1275
AYW	HKVGNFTGLY	54	10	19	95	1276
AYW	KRWGYSNFM	576	10	17	85	1277
AYW	LHLYSHPIIL	490	10	16	80	1278
AYW	LHPAAMPPLL	428	10	20	100	1279
AYW	LHTLWKAGIL	148	10	20	100	1280
AYR	LKLMPARFY	107	10	15	75	1281
AYW	LRRFIILFI	240	10	15	75	1282
AYW	NKTKRWGYSL	573	10	15	75	1283
AYW	NRRVAEDNL	34	10	17	85	1284
AYW	PHHTALROAI	50	10	20	100	1285
AYW	PHLLVGSSGL	434	10	16	80	1286
AYW	QRVGLIGFA	623	10	18	90	1287
AYW	RHYLHTLWKA	145	10	20	100	1288

HBV B27 Super Motif (No binding data available)

TABLE XII

Protein	Sequence	Position in HBV	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SeqID Num
AYW	RKYTSFPWLL	744	10	17	85	1289
AYW	RRAFPHCLAF	527	10	19	95	1290
AYW	RRFIIFLIL	241	10	15	75	1291
AYW	SRKYTSFPWL	743	10	17	85	1292
AYW	SRLWDFSQF	375	10	19	95	1293
AYW	THKVGNTGL	53	10	19	95	1294
AYW	TKRWGYSNLF	575	10	17	85	1295
AYW	TKYLPDCKGI	120	10	20	100	1296
AYW	TRILTIQSL	186	10	16	80	1297
AYW	VHFASPLHVA	819	10	16	80	1298
AYW	VRFWSLSLV	331	10	16	80	1299
AYW	VRAAFPHCLA	526	10	19	95	1300
AYW	WKVCORIVGL	619	10	17	85	1301
AYW	YRWMCURRFI	235	10	19	95	1302
AYW	DHGAHLSLRL	48	11	19	95	1303
AYW	IHLNPNKTRW	568	11	15	75	1304
AYW	IHTAELLAACF	714	11	17	85	1305
AYW	LHPAAMPHLLV	428	11	17	85	1306
AYW	LHTLWKAGILY	148	11	20	100	1307
AYW	LROAILCWGEL	55	11	18	90	1308
AYW	LRRFIIFLIL	240	11	15	75	1309
AYW	PHTALRQAIL	50	11	19	95	1310
AYW	PKFAPNLOSL	394	11	19	95	1311
AYW	PKVLKRTLGL	90	11	17	85	1312
AYW	PRTPARVTGGV	352	11	18	90	1313
AYW	QRVGLLGFAA	623	11	18	90	1314
AYW	RKLPVNRPIDW	609	11	16	80	1315
AYW	RRFIIFILL	241	11	15	75	1316
AYR	RLKLIMPARF	105	11	15	75	1317
AYW	SHPIILGFRKI	494	11	16	80	1318
AYW	SKLQLGWLWGM	20	11	17	85	1319
AYW	SRKYTSFPWLL	743	11	17	85	1320
AYW	THKVGNTGLY	53	11	19	95	1321
AYW	TKRWGYSNLFM	575	11	17	85	1322
AYW	TRHYLTLWKA	144	11	20	100	1323
AYW	VHFASPLHVAW	819	11	16	80	1324
AYW	VRAAFPHCLAF	526	11	19	95	1325
AYW	WKVCORIVGLL	619	11	17	85	1326
AYW	YRWMCURRFII	235	11	19	95	1327

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Table XIII

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
POL	AAMPHLLV	431	8	17	85	1328
NUC	ASALYREA	34	8	17	85	1329
POL	ASFCGSPY	166	8	20	100	1330
NUC	ASKCLGW	19	8	18	90	1331
POL	ASPLHVAW	822	8	16	80	1332
EW	ASVRFSWL	329	8	16	80	1333
POL	ATPTGWGL	690	8	19	95	1334
X	CALRFTSA	69	8	18	90	1335
NUC	CSPHTAL	48	8	20	100	1336
POL	CSWRRAF	523	8	19	95	1337
POL	ESRLWDF	374	8	19	95	1338
NUC	ETVLEYLV	142	8	15	75	1339
POL	FARSRGA	724	8	17	85	1340
POL	FASPLHVA	821	8	16	80	1341
POL	FSPTYKAF	658	8	19	95	1342
X	FSSAGPCA	63	8	19	95	1343
EW	FSWLSLLV	333	8	20	100	1344
POL	FSYMDDW	536	8	18	90	1345
POL	FTOCGYPA	635	8	19	95	1346
POL	FTSAICSV	518	8	19	95	1347
POL	GAKSVOHL	545	8	17	85	1348
POL	GTDNSVL	735	8	18	90	1349
POL	HTAELLAA	715	8	17	85	1350
NUC	HTALRQAI	52	8	20	100	1351
POL	HTLWKAGI	149	8	20	100	1352
POL	LAQFTSAI	515	8	19	95	1353
NUC	LSRLPSDF	45	8	19	95	1354
POL	LSLDVSAA	415	8	19	95	1355
EW	LSLLVPFV	336	8	20	100	1356
X	LSLRGLPV	53	8	19	95	1357
POL	LSRKYTSF	742	8	17	85	1358
POL	LSSNLSWL	408	8	18	90	1359
POL	LSWLSLDV	412	8	20	100	1360
NUC	LTFGRETV	108	8	19	95	1361
X	MSTTDLEA	103	8	16	80	1362
NUC	NAPILSTL	136	8	20	100	1363
POL	PAAMPHLL	430*	8	20	100	1364
POL	PALMPLYA	641	8	19	95	1365
X	PARDVLCL	11	8	16	80	1366
POL	PARVTGGV	355	8	18	90	1367
NUC	PAYRPPNA	130	8	19	95	1368
POL	PSRGRGL	779	8	18	90	1369
POL	PTGWGLAI	692	8	15	75	1370
POL	PTTGRTSL	797	8	17	85	1371
NUC	PTVOASKL	15	8	16	80	1372
EW	PTWLSVI	351	8	15	75	1373

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Table XIII

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
POL	RAFPCHLA	528	8	19	95	1374
X	RTLGLSAM	96	8	24	120	1375
NJC	SALYREAL	35	8	18	90	1376
X	SSAGPCAL	64	8	19	95	1377
EW	SSGTVPV	136	8	15	75	1378
EW	SSKPROGM	5	8	18	90	1379
NJC	STLPETTV	141	8	20	100	1380
X	STTDLEAY	104	8	15	75	1381
NJC	TALROAIL	53	8	19	95	1382
POL	TSAICSVV	519	8	19	95	1383
EW	TSGRIGPL	168	8	16	80	1384
X	TTDLEAYF	105	8	15	75	1385
POL	TTGRTSLY	798	8	17	85	1386
POL	VSWPKFAV	391	8	19	95	1387
NJC	VSYVNVNM	115	8	20	100	1388
POL	VTGGVFLV	358	8	20	100	1389
EW	WSPQAQGI	66	8	17	85	1390
POL	WTHKVGNF	52	8	20	100	1391
POL	YSLNFMGY	580	8	17	85	1392
POL	YTSFPWLL	746	8	17	85	1393
POL	AAPFTQCGY	632	9	19	95	1394
NJC	ASALYREAL	34	9	17	85	1395
NJC	ASKLGLGWL	19	9	18	90	1396
POL	ATPTGWGLA	690	9	16	80	1397
POL	CSRNLVSL	471	9	16	80	1398
POL	DATPTGWGL	689	9	19	95	1399
EW	DSWWTSLNF	196	9	19	95	1400
POL	EAGPLEEL	17	9	20	100	1401
POL	FADATPTGW	687	9	19	95	1402
POL	FASPLHVAW	821	9	16	80	1403
POL	FAVPNLOSL	396	9	19	95	1404
POL	FSPTYKAF	658	9	19	95	1405
X	FSSAGPCAL	63	9	19	95	1406
POL	FSYMDDVL	536	9	18	90	1407
POL	FTFSPTYKA	656	9	19	95	1408
POL	FTGLYSSTV	59	9	18	90	1409
POL	FTCCGYPAL	635*	9	19	95	1410
POL	FTSAICSVV	518	9	19	95	1411
X	GAHLSRGL	50	9	19	95	1412
NJC	HTALROAIL	52	9	19	95	1413
POL	HTLWKAGIL	149	9	20	100	1414
POL	KSVQHLESL	547	9	17	85	1415
POL	KTKRWGYSL	574	9	19	95	1416
POL	LAFSYMDDV	534	9	18	90	1417
NJC	LSFLPSOFF	45	9	19	95	1418
POL	LSLDVSAAF	415	9	19	95	1419

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Table XIII

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
POL	LSPLLAOF	510	9	19	95	1420
EW	LSPTWLSV	349	9	15	75	1421
NUC	LSTLPETTV	140	9	20	100	1422
EW	LSVNPPLGF	16	9	15	75	1423
POL	LSYQHFRKL	3	9	15	75	1424
NUC	LTFGRETVL	137	9	15	75	1425
POL	LTNLSSNL	404	9	18	90	1426
POL	LTVNEKRRL	99	9	17	85	1427
X	MSTTDLEAY	103	9	15	75	1428
POL	NSWLSRKY	738	9	18	90	1429
POL	PAAMPHLLV	430	9	17	85	1430
POL	PARVTGGVF	355	9	18	90	1431
POL	PTTGRTSLY	797	9	17	85	1432
EW	PTWLSVIW	351	9	15	75	1433
POL	QAFIFSPTY	654	9	19	95	1434
NUC	QALLWGEI	57	9	18	90	1435
NUC	QASKLCLGW	18	9	16	80	1436
POL	RAFPCHLAF	528	9	19	95	1437
EW	RTGDPAPNM	167	9	16	80	1438
X	SAGPCALRF	65	9	18	90	1439
POL	SASFCGSPY	165	9	20	100	1440
POL	SNLSWLSL	409	9	18	90	1441
EW	SSSGTNPV	135	9	15	75	1442
NUC	STLPETTV	141	9	20	100	1443
X	STTDLEAY	104	9	15	75	1444
POL	TAELLAACF	716	9	17	85	1445
NUC	TASALYREA	33	9	16	80	1446
POL	TSFVYVPSA	764	9	16	80	1447
EW	TSGLGLPL	168	9	15	75	1448
POL	TGRTSLYA	798	9	17	85	1449
POL	VSIPTWKV	48	9	20	100	1450
EW	WSPQAOGIL	66	9	17	85	1451
EW	WSSKPRQGM	4	9	18	90	1452
POL	YSHPIILGF	493	9	16	80	1453
POL	YSLNFMGYV	580	9	15	75	1454
POL	ASFCGSPYSW	166	10	20	100	1455
NUC	ASKLCLGLWLW	19*	10	17	85	1456
EW	ASVRFWSLSL	329	10	16	80	1457
POL	ATPTGWGLAI	690	10	15	75	1458
X	CAFSSAGPCA	61	10	19	95	1459
EW	CTCIPIPSSW	310	10	20	100	1460
EW	CTIPAQGTSM	298	10	16	80	1461
POL	DATPTGWGLA	689	10	16	80	1462
EW	DSWWTSNLFL	196	10	18	90	1463
NUC	DTASALYREA	32	10	16	80	1464
POL	FAAPFTQGGY	631	10	19	95	1465

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Table XIII

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
BW	FSWLSLLVPF	333	10	20	100	1466
POL	FTFSPTYKAF	656	10	19	95	1467
POL	FTOOGYPALM	635	10	38	190	1468
BW	GSSSGTNPV	134	10	15	75	1469
BW	GTNLSVPNPL	13	10	15	75	1470
POL	GTSFYVPSA	763	10	16	80	1471
POL	HTAELLAACF	715	10	17	85	1472
POL	HTLWKAGILY	149	10	20	100	1473
POL	LAFSYMDDV	534	10	18	90	1474
POL	LSLDVSAAFY	415	10	19	95	1475
BW	LSLLVPFQW	336	10	20	100	1476
X	LSLRGLPVC	53	10	19	95	1477
BW	LSPTWLSVI	349	10	15	75	1478
POL	LSRKYTSFPW	742	10	17	85	1479
POL	LSSNLSWLSL	408	10	18	90	1480
NJC	LSTLPETTV	140	10	20	100	1481
POL	LSWLSLDVSA	412	10	20	100	1482
POL	LSYQHFRKLL	3	10	15	75	1483
BW	LTIQSLDSW	189	10	18	90	1484
X	MSTTDLEAYF	103	10	15	75	1485
POL	PADDFSRGRL	775	10	18	90	1486
BW	PAGGSSSGTV	131	10	18	90	1487
POL	PALMPYACI	641	10	19	95	1488
X	PAPCNFTSA	145	10	15	75	1489
POL	PARVTGGVFL	355	10	18	90	1490
NJC	PAYRPPNAPI	130	10	19	95	1491
POL	PTTGRTSLYA	797	10	17	85	1492
NJC	PTVQASKLCL	15	10	16	80	1493
BW	PTWLSVIWM	351	10	30	150	1494
BW	QAGFLLTRI	179	10	16	80	1495
NJC	QAILCWGELM	57	10	36	180	1496
BW	QAMQWNSTTF	107	10	16	80	1497
NJC	QASKLCLGWL	18	10	16	80	1498
BW	QSLDSWWTSL	193	10	18	90	1499
POL	RTPARVTGGV	353	10	18	90	1500
POL	SAICSVVRR	520	10	19	95	1501
X	SSAGPCALRF	64	10	18	90	1502
POL	TAELLAACFA	716	10	17	85	1503
NJC	TALROAILCW	53	10	19	95	1504
NJC	TASALYREAL	33	10	16	80	1505
POL	TSPFWLLGCA	747	10	15	75	1506
POL	TSFYVPSAL	764	10	16	80	1507
BW	TSGFLGPLLV	168	10	15	75	1508
POL	VAEDUNLGNL	37	10	19	95	1509
POL	YSLNFMGYVI	580	10	15	75	1510
POL	AACFARSRSGA	721	11	17	85	1511

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Table XIII

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
POL	AAPFTOCGYPA	632	11	19	95	1512
EW	ASVRFWSLSLL	329	11	16	80	1513
X	CAFFSAGPCAL	61	11	19	95	1514
X	CALRFTSARRM	69	11	26	130	1515
NUC	CSPHTALROA	48	11	20	100	1516
EW	CTCIPSSWA	310	11	20	100	1517
POL	DATPTGWGLAI	689	11	15	75	1518
NUC	DTASALYREAL	32	11	16	80	1519
POL	ESRLWDFSOF	374	11	19	95	1520
POL	FADATPTGWGL	687	11	19	95	1521
X	FSSAGPCALRF	63	11	18	90	1522
EW	FSWLSLLVPFV	333	11	20	100	1523
POL	FSYMDDWLGA	536	11	18	90	1524
POL	FTFSPYKAFI	656	11	19	95	1525
X	GAHLSLRGLPV	50	11	18	90	1526
POL	GAKSVOHLES	545	11	17	85	1527
POL	GTSFVYVPSAL	763	11	16	80	1528
POL	HTAELLAACFA	715	11	17	85	1529
NUC	HTALROAILCW	52	11	19	95	1530
NUC	ISCLTFGRETV	105	11	18	90	1531
POL	KTKRWGYSLNF	574	11	17	85	1532
POL	LAFSYMDDWVL	534	11	18	90	1533
POL	LAQFSAICSV	515	11	19	95	1534
POL	LSLLVPFQWVF	336	11	20	100	1535
X	LSLRGLPVCAF	53	11	19	95	1536
EW	LSPTVWLSVIW	349	11	15	75	1537
POL	LSRKYSFPWL	742	11	17	85	1538
POL	LSWLSLDVSAA	412	11	19	95	1539
POL	LSYOHFRKILL	3	11	15	75	1540
NUC	LTFGRETVLEY	137	11	15	75	1541
EW	LTIPOSLSWW	189	11	18	90	1542
POL	LTNLLSSNLSW	404	11	18	90	1543
EW	LTRLTIPOS	185	11	16	80	1544
X	PARDVLCIRPV	11	11	15	75	1545
POL	PARVTGGVFLV	355	11	18	90	1546
NUC	PAYRPPNAPIL	130	11	19	95	1547
EW	PTVWLSVWMM	351*	11	28	140	1548
POL	QAFTSPYTKA	654	11	19	95	1549
EW	QAGFFELTRIL	179	11	16	80	1550
NUC	QASKLCGLMW	18	11	15	75	1551
POL	QSLTNLLSSNL	402	11	18	90	1552
POL	RAFPCLAFSY	528	11	19	95	1553
POL	RTPARVTGGVF	353	11	18	90	1554
NUC	RTPPAYRPPNA	127	11	19	95	1555
POL	SAICSVVRRAF	520	11	19	95	1556
POL	SASFSGSPYSW	165	11	20	100	1557

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Table XIII

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
POL	SSNLSWLSLDV	409	11	18	90	1558
POL	TSACSWRRA	519	11	19	95	1559
POL	TSFPWLLGCAA	747	11	15	75	1560
EW	TSGFLGPLVL	168	11	15	75	1561
POL	VSWPKFAVPNL	391	11	19	95	1562
POL	WTHKVGNTGL	52	11	19	95	1563
POL	YTSFPWLLGCA	746	11	15	75	1564

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Table XIV

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NUC	AICWGEL	58	8	18	90	1565
POL	APTCCGY	633	8	19	95	1566
POL	AVPNLOSL	397	8	19	95	1567
EW	CIPSSW	312	8	20	100	1568
NUC	QLGWLWGM	23	8	17	85	1569
EW	CLIFLLVL	253	8	20	100	1570
EW	CLRRFIIF	239	8	19	95	1571
POL	CDRVGLL	622	8	17	85	1572
NUC	DIDPYKEF	31	8	18	90	1573
NUC	DLLDTASA	29	8	17	85	1574
EW	DPVRGLY	122	8	16	80	1575
NUC	DPYKEFGA	33	8	18	90	1576
X	DVLCIRPV	14	8	19	95	1577
X	ELGEERL	122	8	16	80	1578
POL	ELLAACFA	718	8	18	90	1579
EW	FIILFLIL	243	8	16	80	1580
EW	FIILLCI	248	8	16	80	1581
EW	FLGPLVL	171	8	15	75	1582
EW	FLVLIDY	256	8	19	95	1583
POL	FWMLGCA	749	8	15	75	1584
EW	FVGLSPTV	346	8	19	95	1585
EW	FVQWVGL	342	8	19	95	1586
POL	FVYVPSAL	766	8	18	90	1587
POL	GLSPFLA	509	8	19	95	1588
EW	GLSPTWML	348	8	20	100	1589
EW	GMLPVCP	265	8	18	90	1590
EW	GPLLVOA	173	8	19	95	1591
POL	GVGLSPFL	507	8	16	80	1592
POL	HLYSHPII	491	8	16	80	1593
POL	HPAAMPHL	429	8	20	100	1594
EW	IIFLILL	244	8	16	80	1595
POL	IILGFRKI	497	8	16	80	1596
NUC	ILCWGELM	59	8	18	90	1597
EW	ILLCLIF	249	8	20	100	1598
POL	ILRGTSFV	760	8	16	80	1599
EW	ILTIPOS	188	8	19	95	1600
EW	IPISSWA	313	8	20	100	1601
EW	IPOSLSW	191	8	18	90	1602
EW	IPSSWAF	315	8	16	80	1603
POL	IVGLLGA	625	8	18	90	1604
POL	KIPMGVGL	503	8	16	80	1605
NUC	KLCGLMW	21	8	17	85	1606
POL	KLIMPARF	108	8	15	75	1607
POL	KLPVNRPI	610	8	16	80	1608
POL	KVGNFTGL	55	8	19	95	1609
X	KVLHKRTL	91	8	17	85	1610
EW	LIFLLVLL	254	8	20	100	1611

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Table XIV

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
POL	LIMPARFY	109	8	20	100	1612
POL	LLAQFTSA	514	8	19	95	1613
BN	LLCLIFLL	251	8	20	100	1614
NUC	LLDTASAL	30	8	17	85	1615
BN	LLDYOGML	260	8	19	95	1616
POL	LLGCAANW	752	8	16	80	1617
POL	LLGFAAPF	628	8	19	95	1618
BN	LLGWSPOA	63	8	17	85	1619
BN	LLCLIFL	250	8	20	100	1620
BN	LLPIFFCL	378	8	20	100	1621
POL	LLSLGHL	563	8	19	95	1622
POL	LLSSNLWS	407	8	18	90	1623
BN	LLTRILTI	184	8	16	80	1624
POL	LLVGSSGL	436	8	16	80	1625
BN	LLVLOAGF	175	8	19	95	1626
BN	LLVPFVQW	338	8	20	100	1627
POL	LMPLYACI	643	8	19	95	1628
BN	LPIFFCLW	379	8	20	100	1629
POL	LPIHTAEL	712	8	17	85	1630
BN	LOAGFRL	178	8	19	95	1631
POL	LOSLTNLL	401	8	20	100	1632
BN	LVLOAGFF	176	8	19	95	1633
BN	LVPPFVQWF	339	8	20	100	1634
NUC	LVSEGWMI	119	8	18	90	1635
POL	LWDFSQF	377	8	20	100	1636
POL	MPLSYOHF	1	8	20	100	1637
NUC	MQLFHLCL	1	8	15	75	1638
BN	MONNSTTF	109	8	16	80	1639
POL	NLNVSPW	45	8	19	95	1640
POL	NLOSLTNL	400	8	20	100	1641
BN	NLSVPNPL	15	8	15	75	1642
POL	NPNTKRW	571	8	15	75	1643
BN	PIFFCLW	380	8	20	100	1644
POL	PIHTAELL	713	8	17	85	1645
BN	PIPSSWAF	314	8	20	100	1646
BN	POSLSDSW	192	8	18	90	1647
X	PVCAFSSA	59	8	19	95	1648
POL	PVNRPIDW	612	8	17	85	1649
X	QLDPARDV	8	8	16	80	1650
POL	RIVGLGF	624	8	18	90	1651
POL	RLKLIMPA	106	8	15	75	1652
NUC	RPPNAPIL	133	8	20	100	1653
NUC	ROLLWFHI	98	8	18	90	1654
POL	RVAEDLNL	36	8	19	95	1655
POL	RVHFA SPL	818	8	16	80	1656
POL	RVTGGVFL	357	8	20	100	1657
POL	SIPWTHKV	49	8	20	100	1658

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Table XIV

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
POL	SLDVSAAF	416	8	19	95	1659
POL	SUNFMGW	581	8	15	75	1660
POL	SPFLAQF	511	8	19	95	1661
EW	SPOAQIL	67	8	17	85	1662
POL	SPSVPSHL	808	8	17	85	1663
EW	SPTVWLSV	350	8	15	75	1664
POL	SPTYKAFI	659	8	19	95	1665
EW	SVPNPLGF	17	8	15	75	1666
POL	SVQHLESL	548	8	17	85	1667
POL	SWLSRKY	739	8	18	90	1668
NC	TLPETTV	142	8	20	100	1669
POL	TLWKAGIL	150	8	20	100	1670
EW	TPPHGGL	57	8	15	75	1671
POL	TPTGWGLA	691	8	16	80	1672
POL	TOGGYPAL	636	8	19	95	1673
POL	TVNEKRRL	100	8	17	85	1674
EW	TWLSVIW	352	8	15	75	1675
EW	VLDYOGM	259	8	19	95	1676
EW	VLOAGFLL	177	8	19	95	1677
EW	VPRVQWV	340	8	19	95	1678
POL	VPSALNPA	769	8	18	90	1679
NC	VOASKLCL	17	8	16	80	1680
POL	WVLGAKSV	542	8	18	90	1681
POL	WILRGTSF	759	8	16	80	1682
NC	WIRTPPAY	125	8	19	95	1683
POL	WLSLVSVA	414	8	20	100	1684
EW	WLSLLVPF	335	8	20	100	1685
EW	WMCURRFI	237	8	19	95	1686
POL	YLHTLWKA	147	8	20	100	1687
POL	YLPDKGI	122	8	20	100	1688
NC	YLVSEGW	118	8	18	90	1689
POL	YPALMPLY	640	8	19	95	1690
POL	YCHFRKLL	5	8	15	75	1691
POL	AICSVVRRRA	521	9	19	95	1692
NC	AICWGLM	58	9	18	90	1693
POL	ALMPYACI	642	9	19	95	1694
NC	ALROAILCW	54	9	19	95	1695
EW	AMOWNSTTF	108	9	16	80	1696
X	AMSTTDLEA	102	9	15	75	1697
X	APCNFFTSA	146	9	15	75	1698
EW	CIPISSWA	312	9	20	100	1699
EW	CLIFLLVL	253	9	20	100	1700
EW	CLRRFIIL	239	9	19	95	1701
NC	CLTFGRETV	107	9	18	90	1702
EW	CPGYRWML	232	9	20	100	1703
NC	OPTVOASKL	14	9	16	80	1704
X	COLDPARDV	7	9	16	80	1705

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Table XIV

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
NUC	DLDTASAL	29	9	17	85	1706
POL	DUNGLNV	40	9	19	95	1707
X	DPARDVLCL	10	9	16	80	1708
POL	DPSRGLGL	778	9	18	90	1709
POL	DWLGAHSV	541	9	18	90	1710
BW	FIIFILL	243	9	16	80	1711
BW	FILLQLIF	248	9	16	80	1712
BW	FLFILLCL	246	9	16	80	1713
POL	FLAQFTSA	513	9	19	95	1714
POL	FLSLGIHL	562	9	19	95	1715
BW	FLTRLITI	183	9	16	80	1716
BW	FPDHOLDPA	14	9	18	90	1717
POL	FPHCLAFSY	530	9	19	95	1718
POL	FPWLLGCAA	749	9	15	75	1719
BW	FVGLSPTW	346	9	19	95	1720
POL	GLCOVFADA	682	9	17	85	1721
POL	GLLGFAAPF	627	9	19	95	1722
BW	GLLGWSPQA	62	9	17	85	1723
POL	GVGLSPFL	507	9	16	80	1724
NUC	GWIRTPPA	123	9	19	95	1725
POL	HLYVGSSGL	435	9	16	80	1726
X	HLSRGLPV	52	9	18	90	1727
POL	HLYSHPIIL	491	9	16	80	1728
POL	HPAAMPHELL	429	9	20	100	1729
BW	IIFLFIILL	244	9	16	80	1730
POL	ILGFRKIPM	498	9	16	80	1731
BW	ILLCLIFL	249	9	20	100	1732
POL	ILRGTSFY	760	9	16	80	1733
BW	IPIPSWAF	313	9	20	100	1734
BW	IPOSLSWW	191	9	18	90	1735
POL	IVGLLGFAA	625	9	18	90	1736
POL	KLHLYSHPI	489	9	19	95	1737
POL	KLIMPARY	108	9	15	75	1738
POL	KVQORIVGL	620	9	17	85	1739
POL	KVGNFTGLY	55	9	19	95	1740
POL	LLAQFTSAI	514	9	19	95	1741
BW	LLCLIFLV	251	9	20	100	1742
NUC	LLDTASALY	30	9	17	85	1743
POL	LLGCAANWI	752	9	16	80	1744
BW	LLCLIFL	250	9	20	100	1745
BW	LLPIFFCLW	378	9	20	100	1746
NUC	LLSFLPSDF	44	9	19	95	1747
POL	LLSNLSWL	407	9	18	90	1748
BW	LLVLOAGFF	175	9	19	95	1749
BW	LLVPEVQWF	338	9	20	100	1750
NUC	LLWFHISCL	100	9	18	90	1751
BW	LPIFFCLW	379	9	20	100	1752

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Table XIV

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
POL	LPIHTAELL	712	9	17	85	1753
X	LPVCAFESSA	58	9	19	95	1754
POL	LPVNRPIDW	611	9	16	80	1755
EW	LVLIDYQGM	258	9	19	95	1756
EW	LVLQAGFEL	176	9	18	90	1757
EW	LVPFQWFFV	339	9	19	95	1758
EW	MMWYWGPSL	360	9	17	85	1759
POL	NLGNLWISI	42	9	19	95	1760
POL	NLLSSNLW	406	9	18	90	1761
POL	NLOSLTNLL	400	9	20	100	1762
POL	NLSWLSLDV	411	9	18	90	1763
EW	PIFFCLWY	380	9	20	100	1764
POL	PIHTAELLA	713	9	17	85	1765
POL	PIILGFRKI	496	9	16	80	1766
EW	PIPSSWAF	314	9	16	80	1767
POL	PLDKGIKPY	124	9	20	100	1768
POL	PLEELPRL	20	9	19	95	1769
EW	PLPIFFCL	377	9	20	100	1770
EW	PLLVLOAGF	174	9	19	95	1771
POL	PLPHTAEL	711	9	16	80	1772
POL	PMGVLSPF	505	9	16	80	1773
NJC	PPAYRPPNA	129	9	19	95	1774
EW	PHGGLGW	58	9	17	85	1775
X	QLDPARDVL	8	9	16	80	1776
EW	RILTIQSL	187	9	16	80	1777
POL	RIVGLGFA	624	9	18	90	1778
POL	RLWDFSOE	376	9	19	95	1779
POL	RVTGGVRLV	357	9	20	100	1780
EW	SLSWWTSL	194	9	19	95	1781
POL	SLOVSAFY	416	9	19	95	1782
EW	SLLVPPVQW	337	9	20	100	1783
POL	SLNFMGYVI	581	9	15	75	1784
X	SLRGLPVCA	54	9	19	95	1785
EW	SPTVWLSVI	350	9	15	75	1786
EW	SVRFWSLSL	330	9	16	80	1787
EW	TIPQSLDSW	190	9	18	90	1788
POL	TLWKAGILY	150	9	20	100	1789
POL	TPARVTGGV	354	9	18	90	1790
POL	TPTGWGLAI	691	9	15	75	1791
POL	TOCGYPALM	636	9	19	95	1792
NJC	TVOASKLCL	16	9	16	80	1793
EW	TWILSVIWM	352	9	15	75	1794
X	VLCLRPVGA	15	9	19	95	1795
X	VLGGRHKL	133	9	18	90	1796
X	VJHRTLGL	92	9	17	85	1797
EW	VLLDYQGM	259	9	19	95	1798
EW	VLOAGFRL	177	9	19	95	1799

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Table XIV

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
POL	VLRSKYTSF	741	9	17	85	1800
POL	WILRGTSFV	759	9	16	80	1801
POL	WILGCAANW	751	9	16	80	1802
POL	WLSLDVSAA	414	9	19	95	1803
BW	WLSLLVPFV	335	9	20	100	1804
BW	WMCLRRFII	237	9	19	95	1805
POL	WPKFAVPNL	393	9	19	95	1806
NCJ	YLVSGVWI	118	9	18	90	1807
POL	YMDDWLGA	538	9	18	90	1808
POL	YPALMPLYA	640	9	19	95	1809
POL	YCHFRKLL	5	9	15	75	1810
POL	YVPSALNPA	768	9	18	90	1811
POL	AICSVVRAAF	521	10	19	95	1812
POL	APFTQCGYPA	633	10	19	95	1813
POL	AQFSAICSV	516	10	19	95	1814
BW	CIPISSWAF	312	10	20	100	1815
POL	CLAFSYMDDV	533	10	18	90	1816
NCJ	CLGWLWGMID	23	10	17	85	1817
BW	CLRRFIIFL	239	10	15	75	1818
X	COLDPARDVL	7	10	16	80	1819
POL	COIVGGLGF	622	10	17	85	1820
NCJ	DIDPYKEFGA	31	10	18	90	1821
NCJ	DLLDTASALY	29	10	17	85	1822
X	DVLCRLPVGA	14	10	19	95	1823
NCJ	ELLSFLPSDF	43	10	19	95	1824
BW	FIIFLILL	243	10	16	80	1825
BW	FILLCLIFL	248	10	16	80	1826
BW	FLFILLCLI	246	10	16	80	1827
BW	FLGRLVLQA	171	10	15	75	1828
POL	FLLAQFTSAI	513	10	19	95	1829
BW	FPDQOLDPAF	14	10	17	85	1830
POL	FPHCLAFSYM	530	10	19	95	1831
BW	FVGLSPTWIL	346	10	19	95	1832
X	FVLGGORHKL	132	10	18	90	1833
X	GLPVCAFSSA	57	10	19	95	1834
POL	GLSPFLAQF	509	10	19	95	1835
BW	GLSPTWLSV	348	10	15	75	1836
NCJ	GMDIDPYKEF	29	10	17	85	1837
X	GPCALRFTSA	67	10	18	90	1838
POL	GPLEELPRL	19	10	19	95	1839
BW	GPLLVLQAGF	173	10	19	95	1840
POL	GVGLSPFLA	507	10	16	80	1841
NCJ	GWIRTPPAY	123	10	19	95	1842
POL	HLNPNKTKRW	569	10	15	75	1843
POL	HPAAMPHLV	429	10	17	85	1844
POL	HPILLGFRKI	495	10	16	80	1845
POL	IILGFRKIPM	497	10	16	80	1846

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Table XIV

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
BW	ILLCLIFLL	249	10	20	100	1847
POL	ILRGTSFVV	760	10	16	80	1848
NUC	ILSTLPETTV	139	10	20	100	1849
BW	IPISSWAF	313	10	16	80	1850
POL	IPMGVGLSPF	504	10	16	80	1851
POL	IPWTHKVGNF	50	10	20	100	1852
NUC	KLCLGWLWGM	21	10	17	85	1853
POL	KLHLYSHPII	489	10	16	80	1854
POL	KLPVNRPIOW	610	10	16	80	1855
POL	KOAFTSPTY	653	10	19	95	1856
POL	KVCORIVGILL	620	10	17	85	1857
X	KVLHKRTLGL	91	10	17	85	1858
BW	LIFLLVLLDY	254	10	19	95	1859
BW	LLCLIFLLV	251	10	20	100	1860
BW	LLDYQGMLPV	260	10	18	90	1861
POL	LLGCAANWIL	752	10	16	80	1862
BW	LLCLIFLLV	250	10	20	100	1863
BW	LLPIFFCLW	378	10	20	100	1864
NUC	LLSLPSDF	44	10	19	95	1865
BW	LLVLDYQGM	257	10	19	95	1866
BW	LLVLOAGFLL	175	10	18	90	1867
BW	LLVPFQWVF	338	10	19	95	1868
BW	LPIFFCLWVY	379	10	20	100	1869
POL	LPIHTAELLA	712	10	17	85	1870
X	LPKVLHKRTL	89	10	16	80	1871
POL	LPLDKGKPY	123	10	20	100	1872
BW	LVLDDYQGM	258	10	19	95	1873
BW	LVLQAGFLL	176	10	18	90	1874
BW	LVLQAGFLL	360	10	17	85	1875
POL	MMWVWGPSLY	406	10	18	90	1876
BW	NLLSSNLSWL	15	10	15	75	1877
BW	NLSVNPPLGF	571	10	15	75	1878
POL	NPNTKRWGY	47	10	20	100	1879
POL	NVSPWTHKV	616	10	17	85	1880
POL	PIDWKVQORI	380	10	20	100	1881
BW	PIFFCLWYI	713	10	17	85	1882
POL	PIHTAELLA	124	10	20	100	1883
POL	PLDKGKPY	20	10	18	90	1884
POL	PLEEELPRLA	10	10	19	95	1885
BW	PLGFFPDHQL	427	10	20	100	1886
POL	PLHPAAMPHL	377	10	20	100	1887
BW	PLPIFFCLW	174	10	19	95	1888
BW	PLLVLOAGFF	711	10	16	80	1889
POL	PLPIHTAELL	2	10	15	75	1890
POL	PLSYQHFRKL	98	10	17	85	1891
POL	PLTVNEKRRL	505	10	16	80	1892
POL	PMGVGLSPFL	134	10	20	100	1893
NUC	PPNAPILSTL					

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Table XIV

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
POL	PVNRPIWMKV	612	10	17	85	1894
NC	QLLWFHISQL	99	10	18	90	1895
POL	RIVGLLGFAA	624	10	18	90	1896
POL	RLKLMPARE	106	10	15	75	1897
NC	RQAILCWGEL	56	10	18	90	1898
POL	RVHFASPLHV	818	10	15	75	1899
BW	SLVVPFQWVF	337	10	20	100	1900
X	SLRGLPVCAF	54	10	19	95	1901
POL	SLTNLLSSNL	403	10	18	90	1902
NC	SPHTALRQA	49	10	20	100	1903
BW	SPTVWLSVIV	350	10	15	75	1904
BW	SVRFWSLSLL	330	10	16	80	1905
BW	TIPOSLSWV	190	10	18	90	1906
POL	TPARVTGGVF	354	10	18	90	1907
NC	TPPAYRPPNA	128	10	19	95	1908
BW	TPPHGGLLGW	57	10	15	75	1909
POL	VLGAKSVQHL	543	10	17	85	1910
X	VLGGCRHKL	133	10	18	90	1911
BW	VPFVQWPFVL	340	10	19	95	1912
POL	VPNLSLTNL	398	10	19	95	1913
NC	VOASKLQLGW	17	10	16	80	1914
POL	WLSRKYTSF	740	10	17	85	1915
POL	WVRAAFPHCL	525	10	19	95	1916
POL	WLRGTSFVY	759	10	16	80	1917
POL	WLLGCAANWI	751	10	16	80	1918
POL	WLSLDVSAAF	414	10	19	95	1919
NC	WLWGMIDPY	26	10	17	85	1920
BW	WNCLRRFIH	237	10	19	95	1921
BW	WMMWYWGPSL	359	10	17	85	1922
POL	YLHTLWKAGI	147	10	20	100	1923
BW	YOGMLPVCP	263	10	18	90	1924
POL	YOHFRKLILL	5	10	15	75	1925
POL	APFTOGGYPAL	633	11	19	95	1926
POL	AQFSAICSW	516	11	19	95	1927
POL	AVPNLSLTNL	397	11	19	95	1928
BW	CIPISSWAFA	312	11	16	80	1929
POL	CLAFSYMDDV	533	11	18	90	1930
BW	CLFLLVLLDY	253	11	19	95	1931
BW	CLRRFIIFLI	239	11	15	75	1932
NC	CPTVOASKLCL	14	11	16	80	1933
POL	CQRVGLLGFA	622	11	17	85	1934
POL	DLNLGNLNSI	40	11	19	95	1935
NC	ELLSRPSDFH	43	11	19	95	1936
BW	FILLICUILL	248	11	16	80	1937
BW	FLFILLICLI	246	11	16	80	1938
BW	FLVLDYQGM	256	11	19	95	1939
BW	FPAGSSSGTV	130	11	15	75	1940

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Table XIV

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
POL	FPWLLGCAANW	749	11	15	75	1941
X	FVLGGCRHKL	132	11	18	90	1942
POL	FVYVPSALNPA	766	11	18	90	1943
EW	GLSPTWLSVI	348	11	15	75	1944
POL	GPLLEELPRLA	19	11	18	90	1945
EW	GPIVLQAGFF	173	11	19	95	1946
POL	GPLTVNEKRRL	97	11	17	85	1947
X	HLSLRGLPVCA	52	11	18	90	1948
POL	HLVSHPIILGF	491	11	16	80	1949
EW	IIFLFIILLCL	244	11	16	80	1950
EW	ILLCLIFLLV	249	11	20	100	1951
NUC	ILSTLPETTVV	139	11	20	100	1952
EW	ILTIPOSLSW	188	11	18	90	1953
POL	IPMGVGLSPFL	504	11	16	80	1954
POL	IVGLLGAAPF	625	11	18	90	1955
POL	KIPMGVGLSPF	503	11	16	80	1956
POL	KLHLYSHPIIL	489	11	16	80	1957
EW	LLCLIFLLVLL	251	11	20	100	1958
EW	LLGWSPQAQGI	63	11	15	75	1959
EW	LLCLIFLLV	250	11	20	100	1960
EW	LLPIFFCLWVY	378	11	20	100	1961
POL	LLSSNLWSLSL	407	11	18	90	1962
EW	LLVLDYOGML	257	11	19	95	1963
EW	LLVLOAGFLL	175	11	18	90	1964
NUC	LLWFHISCLTF	100	11	17	85	1965
EW	LPIFFCLWVYI	379	11	20	100	1966
POL	LPIHTAELLAA	712	11	17	85	1967
POL	LPLKGIKPY	123	11	20	100	1968
POL	LPVNRPIDWKV	611	11	16	80	1969
EW	LOAGFLLTRI	178	11	16	80	1970
EW	LVPFVQWVGL	339	11	19	95	1971
POL	MPLHLYVGSSGL	433	11	16	80	1972
POL	MPLSYQHFRKL	1	11	15	75	1973
POL	NLGNLWVSPW	42	11	19	95	1974
POL	NLSWLSLDSA	411	11	18	90	1975
POL	NPADDPGRGL	774	11	18	90	1976
EW	NPLGFFPDHQL	9	11	19	95	1977
POL	PIDWVQCORIV	616	11	17	85	1978
POL	PILGFRKIPM	496	11	16	80	1979
NUC	PILSTLPETTV	138	11	20	100	1980
POL	PLHPAAMPHILL	427	11	20	100	1981
EW	PLLPFFCLW	377	11	20	100	1982
EW	PLLVQAGFFL	174	11	18	90	1983
POL	PLPIHTAELLA	711	11	16	80	1984
POL	PLSYQHFRKLL	2	11	15	75	1985
POL	PMGVGLSPFLL	505	11	16	80	1986
NUC	PPAYRPPNAPI	129	11	19	95	1987

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Table XIV

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
BW	POAMQWNSTTF	106	11	16	80	1988
BW	POSLSWWTSL	192	11	18	90	1989
X	QLDPADVLCL	8	11	16	80	1990
POL	QVFADATPTGW	685	11	19	95	1991
POL	RLKLMPARFY	106	11	15	75	1992
POL	RPIDWKVQORI	615	11	16	80	1993
NUC	RPPNAPILSTL	133	11	20	100	1994
NUC	ROALCWGELM	56	11	18	90	1995
NUC	ROLLWFHISCL	98	11	18	90	1996
POL	RVAEDNLGNL	36	11	18	90	1997
POL	RVHFASPLHVA	818	11	15	75	1998
POL	SIPWTHKVGNF	49	11	20	100	1999
BW	SLDSWWTSLNF	194	11	19	95	2000
BW	SLVPPFQWVF	337	11	19	95	2001
NUC	SPEHCSPHHTA	44	11	20	100	2002
POL	SPELLAQFTSA	511	11	19	95	2003
NUC	SPHTALRQAI	49	11	20	100	2004
BW	SPTWLSVIWM	350	11	15	75	2005
BW	SVRFWSLSLV	330	11	16	80	2006
POL	SVLSRKYTSF	739	11	17	85	2007
POL	SVRRAPFHCL	524	11	19	95	2008
POL	TPARVTGGVFL	354	11	18	90	2009
POL	TOCGYPALMPL	636	11	19	95	2010
NUC	TVQASKLCLGW	16	11	16	80	2011
BW	VLLDYQGMLPV	259	11	18	90	2012
POL	VLSRKYTSFPW	741	11	17	85	2013
POL	VPNLSLTNLL	398	11	19	95	2014
NUC	VOASKLCLGWL	17	11	16	80	2015
BW	VQWVFVGLSPTV	343	11	19	95	2016
POL	VVLGAKSVQHL	542	11	16	80	2017
POL	VVRRAPFHCLA	525	11	19	95	2018
POL	WILRGTSFYV	759	11	16	80	2019
POL	WLLGCAANWIL	751	11	16	80	2020
POL	WLSLDVSAFY	414	11	19	95	2021
BW	WLSLLVPVQW	335	11	20	100	2022
BW	WMQLRRFIIL	237	11	19	95	2023
BW	WMWVWVWGPSLY	359	11	17	85	2024
POL	YLHTLWKAGIL	147	11	20	100	2025
POL	YLPDKGIKPY	122	11	20	100	2026
POL	YPALMPLYACI	640	11	19	95	2027

TABLE XV

HBV A01 Motif with Binding Information

Conservancy	Freq.	Protein	Position	Sequence	AA	A*0101	SEQIDNO:
100	20	POL	166	ASFCGSPY	8		2028
90	18	POL	737	NSWLSRKY	10	0.0001	2029
95	19	POL	631	FAAPFTOCGY	10	0.0680	2030
95	19	POL	630	GFAAPFTOCGY	11		2031
75	15	NUC	140	GRETVEY	8		2032
85	17	POL	579	GYSUNFMGY	9		2033
100	20	POL	149	HTLWKAGILY	10	0.1100	2034
95	19	POL	653	KQAFIFSPTY	10	0.0001	2035
85	17	NUC	30	LDTASALY	9	12.0000	2036
95	19	POL	415	LSLDVSAAFY	10	0.0150	2037
75	15	NUC	137	LTFGRETVEY	11		2038
85	17	EW	360	MMWYWGPSLY	10		2039
75	15	X	103	MSITDLEAY	9	0.0810	2040
90	18	POL	738	NSWLSRKY	9	0.8500	2041
100	20	POL	124	PLDKGIKPY	9	0.0005	2042
100	20	POL	124	PLDKGIKPY	10	0.1700	2043
85	17	POL	797	PTTGRTSLY	9	0.2100	2044
100	20	POL	165	SASFCGSPY	9		2045
95	19	POL	416	SLDVSAAFY	9	5.2000	2046
75	15	X	104	STTDLEAY	8		2047
85	17	POL	798	TTGRTSLY	8		2048
95	19	POL	414	WLSLDVSAAFY	11		2049
85	17	EW	359	WMMWYWGPSLY	11	0.3200	2050
95	19	POL	640	YPALMPLY	8		2051
85	17	POL	580	YSLNFMGY	8		2052

Table XVI
HBV A03 Motif With Binding

Conservancy	Freq.	Protein	Position	Sequence	AA	A'0301	SeqID Num
85	17	POL	721	AACFARSR	8	0.0004	2053
85	17	POL	721	AACFARSRSGA	11		2054
95	19	POL	632	AAPFTQCGY	9		2055
95	19	POL	632	AAPFTQCGYPA	11		2056
85	17	POL	722	ACFARSRSGA	10		2057
80	16	POL	688	ADATPTGWGLA	11		2058
90	18	POL	776	ADDPGRGR	8		2059
95	19	POL	529	AFPHCLAF	8		2060
95	19	POL	529	AFPHCLAFSY	10		2061
95	19	X	62	AFSSAGPCA	9		2062
90	18	X	62	AFSSAGPCALR	11		2063
95	19	POL	655	AFTFSPTY	8		2064
95	19	POL	655	AFTFSPTYK	9	0.2600	2065
95	19	POL	655	AFTFSPTYKA	10		2066
95	19	POL	655	AFTFSPTYKAF	11		2067
80	16	ENV	180	AGFLLTR	8		2068
90	18	X	66	AGPCALRF	8		2069
90	18	X	66	AGPCALRFTSA	11		2070
95	19	POL	18	AGPLEEELPR	10	0.0004	2071
95	19	POL	521	AICSVRR	8	-0.0002	2072
95	19	POL	521	AICSVWRA	9		2073
95	19	POL	521	AICSVRRRA	10		2074
95	19	NUC	41	ALESPEHCSPH	11		2075
90	18	POL	772	ALNPADDPSPR	10	0.0003	2076
85	17	X	70	ALRFTSAR	8	0.0047	2077
80	16	ENV	108	AMQWNSTTF	9		2078
80	16	ENV	108	AMQWNSTTFH	10		2079
75	15	X	102	AMSITDLEA	9		2080
85	17	NUC	34	ASALYREA	8		2081
100	20	POL	166	ASFGSPY	8	0.0460	2082
80	16	POL	822	ASPLHVAWR	9		2083
75	15	ENV	84	ASTNRQSGR	9		2084
80	16	POL	690	ATPTGWGLA	9	0.0009	2085
80	16	POL	755	CAANWILR	8		2086
95	19	X	61	CAFSSAGPCA	10		2087
90	18	X	69	CALRFTSA	8		2088
85	17	X	69	CALRFTSAR	9	0.0034	2089
80	16	X	6	CCQLDPAR	8		2090
85	17	POL	723	CFARSRSGA	9		2091

Table XVI
HBV A03 Motif With Binding

Conservancy	Freq.	Protein	Position	Sequence	AA	A'0301	SeqID Num.
75	15	POL	607	CFRKLPIVNR	9		2092
95	19	POL	638	CGYPALMPLY	10		2093
95	19	POL	638	CGYPALMPLYA	11		2094
100	20	ENV	312	CIPISSWA	9		2095
100	20	ENV	312	CIPISSWAF	10		2096
80	16	ENV	312	CIPISSWAF	11		2097
95	19	ENV	253	CLIFLLVLLDY	11	0.0083	2098
90	18	X	17	CLRPVGAESR	10	0.0011	2099
95	19	ENV	239	CLRRFIIF	8		2100
75	15	ENV	239	CLRRFIIF	10		2101
100	20	NUC	48	CSPHHTALR	9	0.0029	2102
100	20	NUC	48	CSPHHTALRQA	11		2103
95	19	POL	523	CSWRRAF	8		2104
95	19	POL	523	CSWRRAPPH	10		2105
100	20	ENV	310	CTCIPSSWA	11		2106
80	16	POL	689	DATPTGWGLA	10		2107
90	18	POL	540	DDVVLGAK	8		2108
90	18	NUC	31	DIDPYKEF	8		2109
90	18	NUC	31	DIDPYKEFGA	10		2110
85	17	NUC	29	DLDDTASA	8		2111
85	17	NUC	29	DLDDTASALY	10	0.0001	2112
85	17	NUC	29	DLDDTASALYR	11	0.0042	2113
95	19	ENV	196	DSWWTSLNF	9	0.0006	2114
85	17	NUC	32	DTASALYR	8	0.0004	2115
80	16	NUC	32	DTASALYREA	10		2116
95	19	X	14	DVLCRLPVGA	10		2117
95	19	POL	418	DVSAAFYH	8		2118
90	18	POL	541	DVVLGAKSVQH	11		2119
95	19	POL	17	EAGPLEELPR	11	-0.0009	2120
90	18	NUC	40	EALSPH	8		2121
90	18	POL	718	ELLAACFA	8		2122
90	18	POL	718	ELLAACFAR	9	0.0002	2123
85	17	POL	718	ELLAACFARSR	11	0.0082	2124
95	19	NUC	43	ELLSFLPSDF	10		2125
95	19	NUC	43	ELLSFLPSDF	11		2126
95	19	NUC	43	ESPEHCSPH	9		2127
95	19	NUC	43	ESPEHCSPHH	10		2128
95	19	POL	374	ESRLWDF	8		2129
95	19	POL	374	ESRLWDFSQF	11		2130

Table XVI
HBV A03 Motif With Binding

Conservancy	Freq.	Protein	Position	Sequence	AA	A'0301	SeqID Num
95	19	NUC	174	ETTVRRR	8	0.0003	2131
80	16	NUC	174	ETTVRRGR	10	0.0003	2132
95	19	POL	631	FAAPFTOOGY	10		2133
85	17	POL	724	FARSRSGA	8		2134
80	16	POL	821	FASPLHVA	8		2135
80	16	POL	821	FASPLHVAVR	10		2136
90	18	ENV	13	FFPDHQLDPA	10		2137
85	17	ENV	13	FFPDHOLDPAF	11		2138
75	15	NUC	139	FGRETVLEY	9		2139
75	15	POL	244	FGVEPSGSH	10		2140
95	19	NUC	122	FGWIRTPPA	10		2141
95	19	NUC	122	FGWIRTPPAY	11		2142
80	16	ENV	248	FILLCLIF	9		2143
80	16	ENV	246	FLFILLCLIF	11		2144
75	15	ENV	171	FLGPLLVLOA	10		2145
95	19	POL	513	FLLAQFTSA	9	0.0006	2146
95	19	POL	562	FLSLGIH	8		2147
95	19	ENV	256	FLVLVDY	8	0.0050	2148
100	20	POL	363	FLVDKNPH	8		2149
95	19	POL	658	FSPTYKAF	8		2150
95	19	X	63	FSSAGPCA	8		2151
90	18	X	63	FSSAGPCALR	10		2152
90	18	X	63	FSSAGPCALRF	11		2153
100	20	ENV	333	FSWLSLLVPF	10	0.0004	2154
90	18	POL	536	FSYMDDWLGA	11		2155
95	19	POL	656	FTFSPTYK	8	0.0100	2156
95	19	POL	656	FTFSPTYKA	9		2157
95	19	POL	656	FTFSPTYKAF	10	0.0004	2158
95	19	POL	635	FTOOGYPA	8		2159
95	19	POL	518	FTSAICSVR	10	0.0003	2160
95	19	POL	518	FTSAICSVRR	11	0.0065	2161
95	19	X	132	FVLGGCRH	8		2162
90	18	X	132	FVLGGCRHK	9	0.0430	2163
90	18	POL	766	FVYVPSALNPA	11		2164
80	16	POL	754	GCAANWILR	9		2165
95	19	POL	630	GFAAPFTOOGY	11		2166
90	18	ENV	12	GFFPDHOLDPA	11		2167
75	15	ENV	170	GFLGPLLVLOA	11		2168
85	17	ENV	61	GGLLGSPOA	10		2169

Table XVI
HBV A03 Motif With Binding

Conservancy	Freq.	Protein	Position	Sequence	AA	A'0301	SeqID Num
100	20	POL	360	GGVFLVDK	8		2170
100	20	POL	360	GGVFLVDKNPH	11		2171
75	15	POL	567	GIHLNPNK	8		2172
75	15	POL	567	GIHLNPNKTK	10	0.0025	2173
75	15	POL	567	GIHLNPNKTKR	11		2174
85	17	POL	682	GLCQVFADA	9	0.0001	2175
95	19	POL	627	GLLGFAAPF	9	0.0006	2176
85	17	ENV	62	GLLGWSPOA	9		2177
95	19	X	57	GLPVCAFSSA	10		2178
95	19	POL	509	GLSPFLLA	8		2179
95	19	POL	509	GLSPFLLAQF	10		2180
85	17	NUC	29	GMDIDPYK	8	0.0006	2181
85	17	NUC	29	GMDIDPYKEF	10	-0.0003	2182
90	18	POL	735	GTDSNVLSR	10	0.0010	2183
90	18	POL	735	GTDSNVLSRK	11	0.0140	2184
80	16	POL	763	GTDFVYVPSA	10		2185
80	16	POL	245	GVFSGSGH	9		2186
100	20	POL	361	GVFLVDKNPH	10		2187
80	16	POL	507	GVGLSPFLA	10		2188
95	19	NUC	123	GWIRTPPA	9		2189
95	19	NUC	123	GWIRTPPAY	10	0.0047	2190
95	19	NUC	123	GWIRTPPAYR	11	0.1900	2191
100	20	NUC	47	HCSPHHTA	8		2192
100	20	NUC	47	HCSPHHTALR	10		2193
80	16	POL	820	HFASPLHVA	9		2194
80	16	POL	820	HFASPLHVAWR	11		2195
95	19	X	49	HGAHLSLR	8		2196
85	17	ENV	60	HGGLLGWSPOA	11		2197
90	18	NUC	104	HISLTFGR	9		2198
75	15	POL	569	HLNPNKTK	8		2199
75	15	POL	569	HLNPNKTKR	9		2200
90	18	X	52	HLSRLGLPVCA	11		2201
80	16	POL	491	HLVSHPIILGF	11		2202
85	17	POL	715	HTAELLAA	8		2203
85	17	POL	715	HTAELLAACF	10		2204
85	17	POL	715	HTAELLAACFA	11		2205
100	20	POL	149	HTLWKAGILY	10	0.0440	2206
100	20	POL	149	HTLWKAGILYK	11	0.5400	2207
95	19	POL	522	ICSVVRRRA	8		2208

Table XVI
HBV A03 Motif With Binding

Conservancy	Freq.	Protein	Position	Sequence	AA	A'0301	SeqID Num
95	19	POL	522	ICSWRRAF	9		2209
95	19	POL	522	ICSWRRAPPH	11		2210
90	18	NUC	32	IDPYKEFGA	9		2211
90	18	POL	617	IDWKVCOR	8		2212
100	20	ENV	381	IFFCLWVY	8		2213
95	19	ENV	255	IFLLVLLDY	9		2214
80	16	POL	734	IGTDSVLSR	11		2215
100	20	ENV	249	ILLCLIF	8		2216
80	16	POL	760	ILRGTSFY	9	0.0440	2217
90	18	NUC	105	ISLTFGR	8	0.0004	2218
90	18	POL	625	IVGLLGFA	8		2219
90	18	POL	625	IVGLLGFAA	9		2220
90	18	POL	625	IVGLLGFAAPF	11		2221
100	20	POL	153	KAGLYKR	8	0.0002	2222
80	16	POL	503	KIPMGVGLSPF	11		2223
75	15	POL	108	KLIMPARF	8		2224
75	15	POL	108	KLIMPARFY	9		2225
80	16	POL	610	KLPVNRPIDWK	11		2226
85	17	POL	574	KTKRWGYSLNF	11		2227
75	15	X	130	KVFLGGCR	9	0.0420	2228
75	15	X	130	KVFLGGCRH	10		2229
95	19	POL	55	KVGNFTGLY	9	0.2100	2230
85	17	POL	720	LAACFARSR	9	0.0058	2231
95	19	X	16	LCLRPVGA	8		2232
90	18	X	16	LCLRPVGAESR	11		2233
95	19	POL	683	LCQVFADA	8		2234
100	20	POL	125	LDKGIKPY	8		2235
100	20	POL	125	LDKGIKPY	9		2236
80	16	X	9	LDPARDVLCRL	11		2237
95	19	ENV	195	LDSWWTSLNF	10		2238
85	17	NUC	31	LDTASALY	8		2239
85	17	NUC	31	LDTASALYR	9	0.0004	2240
80	16	NUC	31	LDTASALYREA	11		2241
95	19	POL	417	LDVSAAFY	8		2242
95	19	POL	417	LDVSAAFYH	9		2243
80	16	ENV	247	LFILLCLIF	10		2244
95	19	POL	544	LGAKSVQH	8		2245
80	16	POL	753	LGCANWILR	10		2246
75	15	POL	566	LGIHLNPNK	9		2247

Table XVI
HBV A03 Motif With Binding

Conservancy	Freq.	Protein	Position	Sequence	AA	A'0301	SeqID Num
75	15	POL	566	LGHLNPNKTK	11		2248
95	19	ENV	172	LGPLLVLQA	9		2249
95	19	ENV	172	LGPLLVLQAGF	11		2250
95	19	EM	254	LIFLLVLLDY	10	0.0022	2251
100	20	POL	109	LIMPARFY	8	-0.0002	2252
90	18	POL	719	LLAACFAR	8	0.0024	2253
85	17	POL	719	LLAACFARSR	10		2254
95	19	POL	514	LLAQFTSA	8		2255
85	17	NUC	30	LLDTASALY	9	0.0013	2256
85	17	NUC	30	LLDTASALYR	10	0.0050	2257
80	16	POL	752	LLGCAANWILR	11		2258
95	19	POL	628	LLGFAAPF	8		2259
85	17	EM	63	LLGWSPQA	8		2260
100	20	ETV	378	LLPIFFCLWVY	11	0.0230	2261
95	19	NUC	44	LLSLPSDF	9		2262
95	19	NUC	44	LLSLPSOFF	10		2263
95	19	ENV	175	LLVLQAGF	8		2264
95	19	ENV	175	LLVLQAGFF	9	0.0006	2265
100	20	ENV	336	LLVPFVQWF	9		2266
85	17	NUC	100	LLWFHISCLTF	11		2267
95	19	NUC	45	LSFLPSDF	8		2268
95	19	NUC	45	LSFLPSOFF	9	0.0006	2269
95	19	POL	415	LSLDVSA	8		2270
95	19	POL	415	LSLDVSAAF	9	0.0004	2271
95	19	POL	415	LSLDVSAAFY	10		2272
95	19	POL	415	LSLDVSAAFYII	11		2273
75	15	POL	564	LSLGIHLNPNK	11		2274
100	20	ENV	336	LSLLVPFVQWF	11		2275
95	19	X	53	LSLRGLPVCA	10		2276
95	19	X	53	LSLRGLPVCAF	11		2277
95	19	POL	510	LSPFLAQF	9		2278
9	5	POL	742	LSRKYTSF	8		2279
95	17	NUC	169	LSTLPETTIVR	11	-0.0009	2280
75	15	ENV	16	LSVPNPLGF	9		2281
100	20	POL	412	LSWLSLDVSA	10	0.0048	2282
100	19	POL	412	LSWLSLDVSA	11		2283
95	15	POL	3	LSYQIIFRK	8		2284
75	15	NUC	137	LTFGRETVLEY	11		2285
85	17	POL	99	LTVNEKRR	8	-0.0002	2286

Table XVI
HBV A03 Motif With Binding

Conservancy	Freq.	Protein	Position	Sequence	AA	A'0301	SeqID Num
95	19	ENV	176	LVLQAGFF	8		2287
100	20	ENV	339	LVPRVQWF	8	0.0028	2288
90	18	NUC	119	LVSGWIR	9		2289
100	20	POL	377	LWDFSQF	8	0.0016	2290
100	20	POL	377	LWDFSQFSR	10		2291
95	19	ENV	238	MCJRRFIIF	9		2292
75	15	ENV	238	MCJRRFIIFL	11		2293
90	18	POL	539	MDDWILGA	8		2294
90	18	POL	539	MDDWLGAK	9		2295
90	18	NUC	30	MDIDPYKEF	9		2296
90	18	NUC	30	MDIDPYKEFGA	11		2297
80	16	POL	506	MGVGLSPF	8		2298
80	16	POL	506	MGVGLSPFLA	11		2299
85	17	ENV	360	MMWYWGPSLY	10	0.0500	2300
80	16	X	103	MSTTDLEA	8		2301
75	15	X	103	MSTTDLEAY	9	0.0008	2302
75	15	X	103	MSTTDLEAYF	10		2303
75	15	X	103	MSTTDLEAYFK	11		2304
95	19	POL	561	NFLSLGIH	9		2305
90	18	NUC	75	NLEDPASR	8	-0.0002	2306
95	19	POL	45	NLNVSIPTWH	10		2307
95	19	POL	45	NLNVSIPTWHK	11	-0.0009	2308
95	15	ENV	15	NLSPNPLGF	10		2309
90	18	POL	411	NLSWLSLDVSA	11		2310
75	15	ENV	215	NSQSPTSNH	9		2311
90	18	POL	738	NSVLSRK	8	0.0006	2312
90	18	POL	738	NSWLSRKY	9	0.0020	2313
100	20	POL	47	NVSIPTWH	8		2314
100	20	POL	47	NVSIPTWHK	9	0.0820	2315
90	18	POL	775	PADDPGRGR	9	0.0008	2316
95	19	POL	641	PALMPLYA	8		2317
75	15	X	145	PAPCNFFTSA	10		2318
80	16	X	11	PARDVLCLR	9	0.0002	2319
90	18	POL	355	PARVTGGVF	9		2320
75	15	ENV	83	PASTNRQSGR	10		2321
95	19	NUC	130	PAYRPPNA	8		2322
90	18	X	68	PCALRFTSA	9		2323
85	17	X	68	PCALRFTSAR	10		2324
75	15	X	147	PONFFTSA	8		2325

Table XVI
HBV A03 Motif With Binding

Conservancy	Freq.	Protein	Position	Sequence	AA	A'0301	SeqID Num
95	19	ENV	15	PDHQLDPA	8		2326
90	18	ENV	15	PDHQLDPAF	9		2327
95	19	POL	512	PFLAQFTSA	10		2328
95	19	POL	634	PFTQOGYP	9		2329
100	20	ENV	233	PGRMMQLR	9	0.0008	2330
95	19	ENV	233	PGRMMQLRR	10	0.0048	2331
95	19	ENV	233	PGRMMQLRRF	11		2332
90	18	POL	616	PIDWKVCQR	9	0.0002	2333
100	20	ENV	380	PIFFCLWVY	9	0.0011	2334
85	17	POL	713	PIHTAELLA	9		2335
85	17	POL	713	PIHTAELLAA	10		2336
80	16	POL	496	PIILGFRK	8		2337
100	20	ENV	314	PIPSSWAF	8		2338
80	16	ENV	314	PIPSSWAF	9		2339
100	20	POL	124	PLDKGIKPY	9	0.0001	2340
100	20	POL	124	PLDKGIKPY	10	0.0002	2341
95	19	POL	20	PLEEELPR	8	0.0002	2342
90	16	POL	20	PLEEELPRLA	10		2343
90	19	ENV	10	PLGFFPDH	8		2344
100	20	POL	427	PLHPAAMPH	9	0.0012	2345
95	19	ENV	174	PLLVLQAGF	9		2346
95	19	ENV	174	PLLVLQAGFF	10		2347
80	16	POL	711	PLPIHTAELLA	11		2348
100	20	POL	2	PLSYQHFR	8	-0.0002	2349
75	15	POL	2	PLSYQHFRK	9	0.0011	2350
85	17	POL	98	PLTVNEKR	8	0.0002	2351
85	17	POL	98	PLTVNEKRR	9	0.0008	2352
80	16	POL	505	PMGVGLSPF	9		2353
85	17	POL	797	PTTGRTSLY	9	0.0001	2354
85	17	POL	797	PTTGRTSLYA	10		2355
95	19	X	59	PVCAFSSA	8		2356
90	18	X	20	PVGAESRGR	9	0.0002	2357
85	17	POL	612	PVNRPIDWK	9	0.0310	2358
95	19	POL	654	QAFTFSPTY	9	0.0030	2359
95	19	POL	654	QAFTFSPTYK	10	0.0450	2360
95	19	POL	654	QAFTFSPTYKA	11		2361
80	16	ENV	179	QAGFLLTR	9		2362
80	16	ENV	107	QAMQWNSTTF	10		2363
80	16	ENV	107	QAMQWNSTTFH	11		2364

Table XVI
HBV A03 Motif With Binding

Conservancy	Freq.	Protein	Position	Sequence	AA	A'0301	SeqID Num
95	19	POL	637	QCGYPALMPLY	11		2365
95	19	POL	517	QFTSAICSVVR	11		2366
75	15	NUC	169	QSPRRRSQSR	11		2367
80	16	POL	189	QSSGILSR	8		2368
95	19	POL	528	RAFPHCIA	8		2369
95	19	POL	528	RAFPHCIAF	9	0.0015	2370
95	19	POL	528	RAFPHCIAFSY	11	0.1200	2371
85	17	NUC	28	RDLLDTASA	9		2372
85	17	NUC	28	RDLLDTASALY	11		2373
95	19	X	13	RDVLCILRPVGA	11		2374
100	20	ENV	332	RFSWLSLLVPF	11		2375
95	19	X	56	RGLPVCAF	8		2376
95	19	X	56	RGLPVCAFSSA	11		2377
100	20	NUC	152	RGFSRRR	8		2378
80	16	POL	762	RGTSFVVVPSA	11		2379
90	18	POL	624	RNGLLG	8		2380
90	18	POL	624	RIVGLLGFA	9		2381
90	18	POL	624	RIVGLLGFAA	10		2382
75	15	POL	106	RLKLMPA	8		2383
75	15	POL	106	RLKLMPAR	9	0.0950	2384
75	15	POL	106	RLKLMPARF	10		2385
75	15	POL	106	RLKLMPARFY	11		2386
75	15	X	128	RLKVFVLGGCR	11		2387
95	19	POL	376	RLVWDFSQF	9	0.0006	2388
95	19	POL	376	RLWDFSQFSR	11	0.2800	2389
95	19	NUC	163	RSRRRTSPR	11	-0.0007	2390
75	15	NUC	167	RSQSPRRR	8		2391
75	15	NUC	167	RSQSPRRR	9		2392
90	18	POL	353	RTPARVTGGVF	11		2393
95	19	NUC	127	RTPPAYRPPNA	11		2394
95	19	NUC	188	RTSPRRR	8	-0.0002	2395
95	19	NUC	188	RTSPRRR	9	0.0054	2396
95	16	POL	818	RVHFASPLH	9		2397
75	15	POL	818	RVHFASPLHVA	11		2398
100	20	POL	357	RVTGGVFIVDK	11	0.0190	2399
90	18	X	65	SAGPCALR	8	-0.0002	2400
90	18	X	65	SAGPCALRF	9	-0.0003	2401
95	19	POL	520	SAICSVVR	8	-0.0002	2402
95	19	POL	520	SAICSWRR	9	0.0058	2403

Table XVI
HBV A03 Motif With Binding

Conservancy	Freq.	Protein	Position	Sequence	AA	A'0301	SeqID Num
95	19	POL	520	SAICSWRRA	10		2404
95	19	POL	520	SAICSWRAF	11		2405
95	18	POL	771	SALNPADDPSP	11	-0.0004	2406
90	20	POI	165	SASFCGSPY	9		2407
100	18	NUC	121	SFGWIRTTPA	11		2408
90	19	NUC	46	SFLPSDF	8		2409
95	15	POL	748	SFPWLIGCA	9		2410
75	15	POL	740	SFPWLLGCAA	10		2411
75	16	POL	765	SFWWPSA	8		2412
80	20	POL	49	SIPWTHKVGNF	11		2413
100	19	ENV	194	SLDSWWTSTINF	11		2414
95	19	POL	416	SLDVSAAF	8		2415
95	19	POL	416	SIQVSAFY	9	0.0016	2416
95	19	POL	416	SLDVSAAFYH	10		2417
75	15	POL	565	SIGHLNPNK	10		2418
100	20	ENV	337	SLLVPFVQWF	10		2419
95	19	X	54	SLRGLPVC	9		2420
95	19	X	54	SLRGLPVCAF	10	0.0004	2421
95	18	X	64	SSAGPCALR	9	0.0080	2422
90	18	X	64	SSAGPCALRF	10	-0.0003	2423
90	19	NUC	170	STIPETTIVR	10	0.0007	2424
95	19	NUC	170	STLPETTIVRR	11	0.0150	2425
95	16	ENV	85	STNRQSGR	8		2426
80	15	X	104	STTDLEAY	8		2427
75	15	X	104	STTDLEAYF	9		2428
75	15	X	104	STTDLEAYFK	10	0.0066	2429
75	15	ENV	17	SVNPLGF	8		2430
90	18	POL	739	SVLSRKY	8	-0.0002	2431
85	17	POL	739	SWLSRKYTSF	11		2432
95	19	POL	524	SWRRAPFH	9	0.1100	2433
85	17	POL	716	TAELLAACF	9		2434
85	17	POL	716	TAELLAACFA	10		2435
85	17	POL	716	TAELLAACFAR	11	0.0006	2436
80	16	NUC	33	TASALYREA	9		2437
100	20	ENV	311	TCIPSSWA	10		2438
100	20	ENV	311	TCIPSSWAF	11		2439
80	16	X	106	TDLEAYFK	8		2440
90	18	POL	736	TDSNVLSR	9		2441
90	18	POL	736	TDSNVLSRK	10	0.0006	2442

Table XVI
HBV A03 Motif With Binding

Conservancy	Freq.	Protein	Position	Sequence	AA	A'0301	SeqID Num
90	18	POL	736	TDNSVVLRSKY	11		2443
75	15	NUC	138	TFGRETVLEY	10		2444
95	19	POL	657	TFSPITYKA	8		2445
95	19	POL	857	TFSPITYKAF	9		2446
100	20	POL	359	TGGVFLVQK	9	0.0007	2447
85	17	POL	799	TGRTSLYA	6		2448
95	19	NUC	171	TLPETTVVR	9	0.0008	2449
95	19	NUC	171	TLPETTVRR	10	0.0007	2450
95	19	NUC	171	TLPETTVRRR	11	0.0005	2451
100	20	POL	150	TLWKAGILY	9	0.1300	2452
100	20	POL	150	TLWKAGILYK	10	5.3000	2453
100	20	POL	150	TLWKAGILYKR	11	0.0082	2454
95	19	POL	519	TSAICSVVR	9	0.0005	2455
95	19	POL	519	TSAICSVRR	10	0.0018	2456
95	19	POL	519	TSAICSVRRA	11		2457
75	15	POL	747	TSPFWLLGCA	10		2458
75	15	POL	747	TSPFWLLGCAA	11		2459
80	16	POL	764	TSFVVVPSA	9		2460
75	15	X	105	TTDLAYF	8		2461
75	15	X	105	TTDLAYFK	9	0.0006	2462
85	17	POL	798	TTGRTSLY	8	0.0004	2463
85	17	POL	798	TTGRTSLYA	9		2464
75	15	ENV	278	TTSTGPOK	8		2465
80	16	NUC	175	TTWVRRGR	9	0.0008	2466
80	16	NUC	176	TWRRRGR	8	0.0003	2467
80	16	NUC	176	TWRRRGRSPR	11		2468
95	19	X	60	VCAFSSAGPCA	11		2469
85	17	POL	621	VOQRNGLLGF	11		2470
100	20	POL	379	VDFSQFSR	8		2471
100	20	POL	362	VFLVDKNPH	9		2472
80	16	X	131	VFLGGOR	8		2473
80	16	X	131	VFLGGCRH	9		2474
75	15	X	131	VFLGGCRHK	10		2475
95	19	X	21	VGAESRGR	8		2476
95	19	POL	626	VGLLGFAA	8		2477
95	19	POL	626	VGLLGFAAPF	10		2478
80	16	POL	508	VGLSPFLA	9		2479
80	16	POL	508	VGLSPFLAQF	11		2480
95	19	POL	56	VGNFTGLY	8		2481

Table XVI
HBV A03 Motif With Binding

Conservancy	Freq.	Protein	Position	Sequence	AA	A'0301	SeqID Num
85	17	POL	96	VGPLTVNEK	9	0.0007	2482
85	17	POL	96	VGPLTVNEKR	10		2483
85	17	POL	96	VGPLTVNEKRR	11		2484
95	19	X	15	VLCLRPVGA	9		2485
95	19	POL	543	VLGAKSVQH	9		2486
90	18	X	133	VLGGORHK	8	0.0150	2487
80	16	ENV	177	VLOAGFFLLTR	11		2488
85	17	POL	741	VLSRKYTSF	9		2489
90	18	NUC	120	VSGWWR	8	0.0040	2490
100	20	POL	48	VSIPTWK	8	0.0130	2491
100	20	POL	358	VTGGVFLVDK	10	0.0390	2492
100	20	POL	378	WDFSQFSR	9	0.0015	2493
90	18	POL	542	VVLGAKSVQH	10		2494
85	17	POL	740	WLSRKYTSF	10	0.0004	2495
95	19	POL	525	VVRRAPFH	8		2496
95	19	POL	525	VVRRAPFHCLA	11		2497
80	16	NUC	177	WRRGRSPR	10	0.0027	2498
80	16	NUC	177	WRRGRSPRR	11		2499
80	16	NUC	102	WFHISCLTF	9		2500
90	16	NUC	102	WFHISCLTFGR	11		2501
85	17	NUC	28	WGMDIDPY	8		2502
85	17	NUC	28	WGMDIDPYK	9	-0.0003	2503
85	17	NUC	28	WGMDIDPYKEF	11		2504
85	17	POL	578	WGYSLNRMGY	10		2505
80	16	POL	759	WILRGTSF	8		2506
80	16	POL	759	WILRGTSFY	10	0.0076	2507
95	19	NUC	125	WIRTPPAY	8	-0.0002	2508
95	19	NX	125	WIRTPPAYR	9	0.0008	2509
90	18	POL	314	WLQFRNSK	8	-0.0002	2510
100	20	POL	414	WLSLDVSA	8		2511
95	19	POL	414	WLSLDVSA	9		2512
95	19	POL	414	WLSLDVSAAF	10		2513
95	19	POL	414	WLSLDVSAAFY	11	0.0034	2514
100	20	ENV	335	WLSLLVPF	8		2515
85	17	RLC	26	WLWGMIDIDPY	10	0.0002	2516
85	17	NUC	26	WLWGMIDIDPYK	11	0.0030	2517
95	19	ENV	237	WMCLRRFIIF	10	0.0004	2518
85	17	ENV	359	WMMWYWGPSLY	11	0.0009	2519
100	20	POL	52	WTHKVGNF	8		2520

Table XVI
HBV A03 Motif With Binding

Conservancy	Freq.	Protein	Position	Sequence	AA	A'0301	SeqID Num
100	20	POL	147	YLHTLWKA	8		2521
100	20	POL	122	YLPLDKGIK	9	0.0001	2522
100	20	POL	122	YLPLDKGIKPY	11	-0.0004	2523
90	18	NUC	118	YLVSGWWIR	10	0.0005	2524
90	18	POL	538	YMDDVVLGA	9	0.0001	2525
90	18	POL	538	YMDDWLGA	10	0.0330	2526
80	16	POL	493	YSHPIILGF	9		2527
80	16	FOL	493	YSHIPILGFR	10		2528
80	16	POL	493	YSHIPILGFRK	11		2529
85	17	POL	580	YSLNFMGY	8	-0.0002	2530
75	15	POL	746	YTSFPWLLGCA	11		2531
90	18	POL	768	YVPSALNPA	9		2532

Table XVII
A11 Motif With Binding Information

Conservancy	Frequency	Protein	Position	Sequence	AA	A*1101	SeqID Num
85	17	POL	721	AACFARSR	8		2533
95	19	POL	632	AAPFTOCGY	9		2534
90	18		776	ADDFSRGR	8		2535
95	19	POL	529	AFPHCLAFSY	10		2536
90	19	X	62	AFSSAGPCALR	11		2537
95	19	POL	655	AFTFSPTY	8		2538
95	19	POL	655	AFTFSPTYK	9		2539
80	16	ENV	180	AGFFLLTR	8		2540
95	19	POL	18	AGPLEEELPR	10		2541
95	19	POL	521	AICSVWRR	8		2542
95	19	NUC	41	ALESPEHCSPH	11		2543
90	18	POL	772	ALNPADDPSPR	10		2544
85	17	X	70	ALRFTSAR	8		2545
80	16	ENV	108	AMQWNSTTFH	10		2546
80	8	POL	166	ASFQGGPY	8		2547
80	16	POL	822	ASPLHVAWR	9		2548
75	15	ENV	84	ASTNROSQR	9		2549
80	16	POL	755	CAANWILR	8		2550
85	17	X	69	CALRFTSAR	9		2551
80	16	X	6	CCQLDPAR	8		2552
75	15	POL	607	CFRKLPVNR	9		2553
95	19	POL	638	CGYPALMPY	10		2554
95	19	ENV	253	CLIFLLVLDY	11		2555
90	18	X	17	CLRPVGAESR	10		2556
100	20	NUC	48	CSPHTALR	9		2557
95	19	POL	523	CSVRRAPPH	10		2558
90	18	POL	540	DDVVLGAK	8		2559
85	17	NUC	29	DLDDTASALY	10		2560
85	17	NUC	29	DLDDTASALYR	11		2561
90	18	POL	737	DNSVLSR	8		2562
90	18	POL	737	DNSWLSRK	9		2562
90	18	POL	737	DNSWLSRKY	10		2563
85	17	NUC	32	DTASALYR	8		2564
95	19	POL	418	DVSAAFYH	8		2565
90	18	POL	541	DVVLGAKSVQH	11		2566
95	19	POL	17	EAGPLEEELPR	11		2567
90	18	NUC	40	EALSPH	8		2568
90	18	POL	718	ELLAACFAR	9		2569
85	17	POL	718	ELLAACFARSR	11		2570

Table XVII
A11 Motif With Binding Information

Conservancy	Frequency	Protein	Position	Sequence	AA	A*1101	SeqID Num
95	19	NUC	43	ESPEHCSPH	9		2541
95	19	NUC	43	ESPEHCSPHH	10		2542
95	19	NUC	174	ETTVRRR	8		2543
80	16	NUC	174	ETTVRRRRGR	10		2544
95	19	POL	631	FAAPFTOOGY	10		2545
80	16	POL	821	FASPLHVAWR	10		2546
75	15	NUC	139	FGRETVLEY	9		2547
75	15	POL	244	FGVEPSCSGH	10		2548
95	19	NUC	122	FGWIRTPPAY	11		2549
95	19	POL	562	FLLSLGIH	8		2550
95	19	ENV	256	FLLVLLDY	8		2551
100	20	POL	363	FLVDKVPH	8		2552
90	18	X	63	FSSAGPCALR	10		2553
95	19	POL	656	FTFSPTYK	8		2554
95	19	POL	518	FTSAICSWR	10		2555
95	19	POL	518	FTSAICSWRR	11		2556
95	19	X	132	FVLGGGRH	8		2557
90	18	X	132	FVLGGGRHK	9		2558
80	16	POL	754	GCAANWILR	9		2559
95	19	POL	630	GFAAPFTOOGY	11		2560
100	20	POL	360	GGVFLVDK	8		2561
100	20	POL	360	GGVFLVDKNPH	11		2562
75	15	POL	567	GIHLNPNK	8		2563
75	15	POL	567	GIHLNPNKTK	10		2564
75	15	POL	567	GIHLNPNKTKR	11		2565
85	17	NUC	29	GMDIDPYK	8		2566
95	19	POL	44	GNLNVSIPTWTH	11		2567
90	18	POL	735	GTDNVSVLSR	10		2568
90	18	POL	735	GTDNVSVLSRK	11		2569
80	16	POL	245	GVEPSCSGH	9		2570
100	20	POL	361	GVFLVDKNPH	10		2571
95	19	NUC	123	GWIRTPPAY	10		2572
95	19	NUC	123	GWIRTPPAYR	11		2573
100	20	NUC	47	HCSPHHTALR	10		2574
80	16	POL	820	HFASPLHVAWR	11		2575
95	19	X	49	HGAHLSLR	8		2576
90	18	NUC	104	HISLITGR	9		2577
75	15	POL	569	HLNPNKTK	8		2578
75	15	POL	569	HLNPNKTKR	9		2579

Table XVII
A11 Motif With Binding Information

Conservancy	Frequency	Protein	Position	Sequence	AA	A*1101	SeqID Num
100	20	POL	149	HTLWKAGILY	10		2580
100	20	POL	149	HTLWKAGILYK	11		2581
95	19	POL	522	ICSWRRAPFH	11		2582
90	18	POL	617	IDWKVCOR	8		2583
100	20	ENV	381	IFFQLWY	8		2584
95	19	ENV	255	IFLLVLLDY	9		2585
80	16	POL	734	IGTDNSVLSR	11		2586
80	16	POL	760	ILRGTSFY	9		2587
90	18	NUC	105	ISLTFGR	8		2588
100	20	POL	153	KAGILYKR	8		2589
75	15	POL	108	KLMPARFY	9		2590
80	16	POL	610	KLPVNRPIDWK	11		2591
75	15	X	130	KVFLGGCR	9		2592
75	15	X	130	KVFLGGCRH	10		2593
95	19	POL	55	KVGNFTGLY	9		2594
85	17	POL	720	LAACFARS	9		2595
90	18	X	16	LCRPVGAESR	11		2596
100	20	POL	125	LDKGIKPY	8		2597
100	20	POL	125	LDKGIKPY	9		2598
80	16	X	9	LDPARDVLCILR	11		2599
85	17	NUC	31	LDTASALY	8		2600
85	17	NUC	31	LDTASALYR	9		2601
95	19	POL	417	LDVSAAFY	8		2602
95	19	POL	417	LDVSAAFYH	9		2603
95	19	POL	544	LGAKSVQH	8		2604
80	16	POL	753	LGAANWILR	10		2605
75	15	POL	566	LGIHLNPNK	9		2606
75	15	POL	566	LGIHLNPNKTK	11		2607
95	19	ENV	254	LIFLLVLLDY	10		2608
100	20	POL	109	LIMPARFY	8		2609
90	18	POL	719	LLAACFAR	8		2610
85	17	POL	719	LLAACFARSR	10		2611
85	17	NUC	30	LLDTASALY	9		2612
85	17	NUC	30	LLDTASALYR	10		2613
80	16	POL	752	LLGCAANWILR	11		2614
100	20	ENV	378	LLPIFFCLWY	11		2615
90	18	POL	773	LNPAADPSR	9		2616
90	18	POL	773	LNPAADPSRGR	11		2617
75	15	POL	570	LNPNTKR	8		2618

Table XVII
A11 Motif With Binding Information

Conservancy	Frequency	Protein	Position	Sequence	AA	A*1101	SeqID Num
75	15	POL	570	LNPNTKRWGY	11		2619
95	19	POL	46	LNVSIPWTH	11		2620
95	19	POL	46	LNVSIPWTHK	10		2621
95	19	POL	415	LSLDVSAFY	10		2622
95	19	POL	415	LSLDVSAFYH	11		2623
75	15	POL	564	LSGLHLPNK	11		2624
95	19	NUC	169	LSTLPETTVR	11		2625
75	15	POL	3	LSYQHFRK	8		2626
75	15	NUC	137	LTFGRETVLEY	11		2627
85	17	POL	99	LTVNEKRR	8		2628
90	18	NUC	119	LVFSGWIR	9		2629
100	20	POL	377	LVDFSOFSR	10		2630
90	18	POL	539	MDDVVLGAK	9		2631
85	17	ENV	360	MMWYWGPLY	10		2632
75	15	X	103	MSTTDLEAY	9		2633
75	15	X	103	MSTTDLEAYFK	11		2634
95	19	POL	561	NFLSLGIH	9		2635
90	18	NUC	75	NLEDPASR	8		2636
95	19	POL	45	NLNVSIPTWTH	10		2637
95	19	POL	45	NLNVSIPTWTHK	11		2638
75	15	ENV	215	NSQSPSTNH	9		2639
90	18	POL	738	NSVLSRK	8		2640
90	18	POL	738	NSVLSRKY	9		2641
100	20	POL	47	NVSIPTWTH	8		2642
100	20	POL	47	NVSIPTWTHK	9		2643
90	18	POL	775	PADDPGRGR	9		2644
80	16	X	11	PARDVLCIR	9		2645
75	15	ENV	83	PASTNROSGR	10		2646
85	17	X	68	PCALFTSAR	10		2647
100	20	ENV	233	PGYRMMLQR	9		2648
95	19	ENV	233	PGYRMMLRR	10		2649
90	18	POL	616	PIDWKVQQR	9		2650
100	20	ENV	380	PIFFCLWY	9		2651
80	16	POL	496	PILGFRK	8		2652
100	20	POL	124	PLDKGIKPY	9		2653
100	20	POL	124	PLDKGIKPY	10		2654
95	19	POL	20	PLEELPR	8		2655
95	19	POL	10	PLGFFPDH	8		2656
100	20	POL	427	PLHPAAMPH	9		2657

Table XVII
A11 Motif With Binding Information

Conservancy	Frequency	Protein	Position	Sequence	AA	A*11101	SeqID Num
100	20	POL	2	PLSYQHFR	8		2658
75	15	POL	2	PLSYQHFRK	9		2659
85	17	POL	98	PLTVNEKR	8		2660
85	17	POL	98	PLTVNEKRR	9		2661
75	15	POL	572	PNKTRWGY	9		2662
85	17	POL	797	PTTGRTSLY	9		2663
90	18	X	20	PVGAESRGR	9		2664
85	17	POL	612	PVNRPIDWK	9		2665
95	19	POL	654	QAFTFSPTY	9		2666
95	19	POL	654	QAFTFSPTYK	10		2667
80	16	ENV	179	QAGFLLTR	9		2668
80	16	ENV	107	QAMQWNSTTFH	10		2669
95	19	POL	637	QCGYPALMPY	11		2670
95	19	POL	517	QFTSAICSVWR	11		2671
75	15	NUC	169	QSPRRRSQSR	11		2672
80	16	POL	189	QSSGILSR	8		2673
95	19	POL	528	RAFPHCIAFSY	11		2674
85	17	NUC	28	RDLLDTASALY	11		2675
100	20	NUC	152	RCFSRRRR	8		2676
75	15	POL	106	RLKLIMPAR	9		2677
75	15	POL	106	RLKLIMPARIFY	11		2678
75	15	X	128	RLKVFVLGGR	11		2679
95	19	POL	376	RLWDFSQFSR	11		2680
95	19	NUC	183	RSPRRRTPSRR	11		2681
75	15	NUC	167	RSOSRRRR	8		2682
75	15	NUC	167	RSOSRRRRR	9		2683
95	19	NUC	188	RTPSPRRR	8		2684
95	19	NUC	188	RTPSPRRRR	9		2685
80	16	POL	818	RVHFA SPLH	9		2686
100	20	POL	357	RVTGGVFLVDK	11		2687
90	18	X	65	SAGPCALR	8		2688
95	19	POL	520	SAICSVWR	8		2689
95	19	POL	520	SAICSWRR	9		2690
90	18	POL	771	SALNPADDP SR	11		2691
100	20	POL	165	SASFGSPY	9		2692
95	19	POL	416	SLDVSAAFY	9		2693
95	19	POL	416	SLDVSAAFYH	10		2694
75	15	POL	565	SLGHLNPNK	10		2695
90	18	X	64	SSAGPCALR	9		2696

Table XVII
A11 Motif With Binding Information

Conservancy	Frequency	Protein	Position	Sequence	AA	A*1101	SeqID Num
95	19	NUC	170	STLPETTWR	10		2697
95	19	NUC	170	STLPETTWR	11		2698
80	16	ENV	85	STNRQGR	8		2699
75	15	X	104	STTDLEAY	8		2700
75	15	X	104	STTDLEAYFK	10		2701
90	18	POL	739	SVLSRKY	8		2702
95	19	POL	524	SWRRAPPH	9		2703
85	17	POL	716	TAELLAACFAR	11		2704
80	16	X	106	TDLEAYFK	8		2705
90	18	POL	736	TDNSVLSR	9		2706
90	18	POL	736	TDNSVLSRK	10		2707
90	18	POL	736	TDNSVLSRK	11		2708
75	15	NUC	138	TFGRETVEY	10		2709
100	20	POL	359	TGGVFLVDK	9		2710
95	19	NUC	171	TLPETTVR	9		2711
95	19	NUC	171	TLPETTVRR	10		2712
95	19	NUC	171	TLPETTVRRR	11		2713
100	20	POL	150	TLWKAGILY	9		2714
100	20	POL	150	TLWKAGILYK	10		2715
100	20	POL	150	TLWKAGILYKR	11		2716
95	19	POL	560	TNFLSLGIH	10		2717
95	19	POL	519	TSAICSWR	9		2718
95	19	POL	519	TSAICSWRR	10		2719
75	15	X	105	TTDLEAYFK	9		2720
85	17	POL	798	TTGRTSLY	8		2721
75	15	ENV	278	TTSTGPK	8		2722
80	16	NUC	175	TTWRRGR	9		2723
80	16	NUC	176	TTWRRGR	8		2724
80	16	NUC	176	TTWRRGRSPR	11		2725
100	20	POL	379	VDFSQFSR	8		2726
100	20	POL	362	VFLVDKNPH	9		2727
80	16	X	131	VFLGGGR	8		2728
80	16	X	131	VFLGGGRH	9		2729
75	15	X	131	VFLGGGRHK	10		2730
95	19	X	21	VGAESGR	8		2731
95	19	POL	56	VGNFTGLY	8		2732
85	17	POL	96	VGPLTVNEK	9		2733
85	17	POL	96	VGPLTVNEKR	10		2734
85	17	POL	96	VGPLTVNEKR	11		2735

Table XVII
A11 Motif With Binding Information

Conservancy	Frequency	Protein	Position	Sequence	AA	A*1101	SeqID Num
95	19	POL	543	VLGAKSVQH	9		2736
90	18	X	133	VLGGQRHK	8		2737
80	16	ENV	177	VLOAGFFLTR	11		2738
85	17	POL	613	VNRPIDWK	8		2739
90	18	NUC	120	VSGFWIR	8		2740
100	20	POL	48	VSIPWTHK	8		2741
100	20	POL	358	VTGGVFLVDK	10		2742
100	20	POL	378	VWFSQFSR	9		2743
90	18	POL	542	VLGAKSVQH	10		2744
95	19	POL	525	VWRAFFPH	8		2745
80	16	NUC	177	WRRRGSPRR	10		2746
80	16	NUC	177	WRRRGSPRR	11		2747
90	18	NUC	102	WFHISCLTFR	11		2748
85	17	NUC	28	WGMDIDPY	8		2749
85	17	NUC	28	WGMDIDPYK	9		2750
85	17	POL	578	WGYSUNRMGY	10		2751
80	16	POL	759	WILGTSPVY	10		2752
95	19	NUC	125	WIRTPPAY	8		2753
95	19	NUC	125	WIRTPPAYR	9		2754
90	18	POL	314	WLQFRNSK	8		2755
95	19	POL	414	WLSLDVSAIFY	11		2756
85	17	NUC	26	WLWGMDIDPY	10		2757
85	17	NUC	26	WLWGMDIDPYK	11		2758
85	17	ENV	359	WMMWYWGPSLY	11		2759
100	20	POL	122	YLPDKGIK	9		2760
100	20	POL	122	YLPDKGIKPY	11		2761
90	18	NUC	118	YLVSGWIR	10		2762
90	18	POL	538	YMDDVVLGAK	10		2763
80	16	POL	493	YSHPIILGFR	10		2764
80	16	POL	493	YSHPIILGFRK	11		2765
85	17	POL	580	YSUNRMGY	8		2766

HBV A24 Motif With Binding Information

Table XVIII

Conservancy	Freq.	Protein	Position	Sequence	SEQ ID NO:	AA	Filed	A*2401
95	19	POL	529	AFPHCLAF	2767	8		
95	19	X	62	AFSSAGPCAL	2768	10		0.0012
90	18	POL	535	AFSYMDDWL	2769	10		0.0009
95	19	POL	655	AFTFSPTYKAF	2770	11		
80	16	ENV	108	AMQWNSTTF	2771	9		
100	20	NUC	131	AYRPPNAPI	2772	9		0.0310
100	20	NUC	131	AYRPPNAPIL	2773	10		0.0042
75	15	POL	607	CFRKLPNRPI	2774	11		
85	17	POL	618	DMKVCQRI	2775	8		
85	17	POL	618	DMKVCQRI	2776	11		
90	18	ENV	262	DYOGMLPVCPL	2777	11		0.0002
90	18	NUC	117	EYLVSGVW	2778	9		
90	18	NUC	117	EYLVSGVWI	2779	10		
100	20	ENV	382	FFCLWYI	2780	8		
80	16	ENV	182	FFLLTRIL	2781	8		
80	16	ENV	182	FFLLTRILTI	2782	10		
85	17	ENV	13	FFPDHQLDPAF	2783	11		
80	16	ENV	181	GFLLTRI	2784	8		
80	16	ENV	181	GFLLTRIL	2785	9		
80	16	ENV	181	GFLLTRILTI	2786	11		
95	19	ENV	12	GFFPDHQL	2787	8		
75	15	ENV	170	GFLGPLVL	2788	9		
80	16	POL	500	GFRKIPMGVGL	2789	11		
85	17	NUC	29	GMDIDPYKEF	2790	10		
90	18	ENV	265	GMLPVCPL	2791	8		
85	17	NUC	25	GWLWGMDI	2792	8		
85	17	ENV	65	GWSPQAOGI	2793	9		0.0024
85	17	ENV	65	GWSPQAOGIL	2794	10		0.0003
95	19	POL	639	GYPALMPL	2795	8		0.0007
95	19	ENV	234	GYRWMCLRRF	2796	10		
95	19	ENV	234	GYRWMCLRRFI	2797	11		
75	15	POL	579	GYSNFMGYVI	2798	11		
80	16	POL	820	HFASPLHVAW	2799	10		
75	15	POL	7	HFRKLILL	2800	8		
100	20	POL	146	HYLHTLWKAGI	2801	11		
100	20	ENV	381	IFFCLWYI	2802	9		0.0087
80	16	ENV	245	IFLFIILL	2803	8		
80	16	ENV	245	IFLFIILLCL	2804	10		
80	16	ENV	245	IFLFIILLCL	2805	11		
85	17	ENV	358	IWMWYWGPSL	2806	11		0.0004
95	19	POL	395	KFAVPLNLSL	2807	10		0.0020
100	20	POL	121	KYLPDKGI	2808	9		
85	17	POL	745	KYTSFPWL	2809	8		

Table XVIII
HBV A24 Motif With Binding Information

Conservancy	Freq.	Protein	Position	Sequence	SEQ ID NO:	AA	Filed	A*2401
85	17	POL	745	KYTSFPWLL	2810	9	.	5.3000
80	16	EN	247	LFILLCL	2811	8	.	
80	16	EN	247	LFILLCLI	2812	9	.	
80	16	EN	247	LFILLCLUF	2813	10	.	
80	16	EN	247	LFILLCLIFL	2814	11	.	
95	19	POL	643	LMPYACI	2815	8	.	
90	18	NUC	101	LWFHISCL	2816	8	.	
85	17	NUC	101	LWFHISCLTF	2817	10	.	
80	16	POL	492	LYSHPIIL	2818	8	.	
80	16	POL	492	LYSHPIILGF	2819	10	.	
85	17	EN	360	MMWYWGPSL	2820	9	.	1.1000
85	17	EN	361	MMWYWGPSL	2821	8	.	0.0060
95	19	POL	561	NFLSLGI	2822	8	.	0.0005
95	19	POL	561	NFLSLGIHL	2823	10	.	0.0099
80	16	POL	758	NWILRGTSF	2824	9	.	
95	19	POL	512	PFLLAQFTSAI	2825	11	.	
95	19	POL	634	PFTGGYPAL	2826	10	.	0.0002
95	19	EN	341	PFVQWVGL	2827	9	.	0.0003
80	16	POL	505	PMGVGLSPF	2828	9	.	
80	16	POL	505	PMGVGLSPFL	2829	10	.	
80	16	POL	505	PMGVGLSPFL	2830	11	.	
80	16	POL	750	PWLLGCAANW	2831	10	.	
80	16	POL	750	PWLLGCAANWI	2832	11	.	
100	20	POL	51	PWTHKVGNF	2833	9	.	0.0290
95	19	EN	344	QWVGLSPTW	2834	11	.	
75	15	EN	242	RFIIFLI	2835	8	.	
75	15	EN	242	RFIIFLFI	2836	9	.	
75	15	EN	242	RFIIFLFI	2837	10	.	
75	15	EN	242	RFIIFLFI	2838	11	.	
100	20	EN	332	RFSWLSLL	2839	8	.	
100	20	EN	332	RFSWLSLLVPF	2840	11	.	
85	17	POL	577	RMGYSUNF	2841	8	.	
95	19	EN	236	RWMCLRRF	2842	8	.	
95	19	EN	236	RWMCLRRFI	2843	9	.	0.0710
95	19	EN	236	RWMCLRRFI	2844	10	.	1.1000
95	19	EN	236	RWMCLRRFI	2845	11	.	
100	20	POL	167	SFCGSPYSW	2846	9	.	0.0710
95	19	NUC	46	SFLPSDF	2847	8	.	
80	16	POL	765	SFYVPSAL	2848	9	.	
95	19	POL	413	SWLSLDVSAAF	2849	11	.	
100	20	EN	334	SWLSLLVPF	2850	9	.	0.3900
95	19	POL	392	SWPKFAVPNL	2851	10	.	5.6000
100	20	EN	197	SWWTSUNF	2852	8	.	

HBV A24 Motif With Binding Information

Table XVIII

Conservancy	Freq.	Protein	Position	Sequence	SEQ ID NO.	AA	Filed	A*2401
95	19	EW	197	SWWTSLNFL	2853	9	.	0.3800
90	18	POL	537	SYMDVDVL	2854	8	.	
75	15	POL	4	SYQHFRKL	2855	8	.	
75	15	POL	4	SYQHFRKLL	2856	9	.	0.0051
75	15	POL	4	SYQHFRKLL	2857	10	.	0.0660
75	15	POL	4	SYQHFRKLL	2858	11	.	
75	15	NUC	138	TGRETIVL	2859	8	.	
75	15	NUC	138	TGRETIVLYL	2860	11	.	
95	19	POL	657	TFSPYKAF	2861	9	.	0.0060
95	19	POL	657	TFSPYKAF	2862	10	.	0.0043
95	19	POL	686	VFADATPTGW	2863	10	.	0.0180
75	15	X	131	VFLGGCRHKL	2864	11	.	
90	18	NUC	102	WFHISCLTF	2865	9	.	0.0300
95	19	EW	345	WFGVLSPTW	2866	10	.	0.0120
95	19	EW	345	WFGVLSPTW	2867	11	.	
95	19	EW	237	WMCLRRFI	2868	8	.	
95	19	EW	237	WMCLRRFI	2869	9	.	
95	19	EW	237	WMCLRRFIIF	2870	10	.	0.0013
95	19	EW	237	WMCLRRFIIFL	2871	11	.	
85	17	EW	359	WMWWWGPSL	2872	10	.	
95	19	EW	198	WWTSLNFL	2873	8	.	

Table XIXa

HBV DR-SUPER MOTIF

Protein	Core SEQ ID NO:	Core Sequence	Core Freq.	Core Conservancy (%)	Exemplary SEQ ID NO:	Exemplary Sequence	Position in HBV Poly-Protein	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
POL	2874	FAAFTQGG	19	95	3021	LLGFAAPFTQCGYPA	628	19	95
POL	2875	FADATPTGW	19	95	3022	COVFADATPTGWGLA	684	16	80
POL	2876	FAVFNLSL	19	95	3023	WPKFAVFNLSLTNL	393	19	95
NJC	2877	FGRETVEY	15	75	3024	CLTFGRETVEYLVLS	136	14	70
POL	2878	FGVEPSGG	15	75	3025	RRSFGVEPSGGHID	252	6	30
NJC	2879	FHISCLTFG	18	90	3026	LLWFHISCLTFGRET	100	17	85
NJC	2880	FHLCLISC	16	80	3027	MOLFHLCLISCSCP	1	10	50
EW	2881	FILLCLIF	16	80	3028	IFLILLCLIFLLV	245	16	80
EW	2882	FLILLCLL	16	80	3029	FIIFLILLCLIFL	243	16	80
EW	2883	FLGLVLQ	15	75	3030	TSGFLGLVLQAGF	168	15	75
EW	2884	FLTRILTI	16	80	3031	AGFLLTRILTIPOS	180	16	80
EW	2885	FLVLIDYQ	19	95	3032	CLIFLLVLIDYQGM	253	19	95
EW	2886	FPAGSSGG	15	75	3033	GLYFPAGSSGGTN	127	11	55
EW	2887	FPQHLDPA	18	90	3034	LGFFPDHQLDPAFGA	22	9	45
POL	2888	FPHCLAFSY	19	95	3035	RRAFPCHCLAFSYMDD	527	19	95
POL	2889	FRKIPMGVG	16	80	3036	ILGFRKIPMGVGLSP	498	13	65
POL	2890	FRKLPVNRP	16	80	3037	KOCFRKLPVNRPIDW	616	9	45
X	2891	FSSAGPCAL	19	95	3038	VCAFFSAGPCALRFT	60	18	90
EW	2892	FSWLSLLVP	20	100	3039	SVRFWSWLSLLVPVQ	330	16	80
POL	2893	FTSPITYKA	19	95	3040	KOAFSTPITYKAFCL	653	12	60
POL	2894	FTGLYSSTV	18	90	3041	VGNFTGLYSSTVPVF	56	11	55
POL	2895	FTSAICSW	19	95	3042	LAQFTSAICSWVRR	515	19	95
EW	2896	FVGLSPTW	19	95	3043	VQWVGLSPTWLSV	343	14	70
X	2897	FVLGGGRHK	18	90	3044	LKPVFVLGGGRHKVC	129	14	70
EW	2898	FVQVFGLS	19	95	3045	LVPEVQVQVFGLSPTV	339	19	95
POL	2899	FVVPFSALN	18	90	3046	GTSFVVPFSALNPAD	763	18	80
POL	2900	IDWKVCORI	17	85	3047	NRPIDWKVCORIVGL	614	16	80
EW	2901	IFLILLCL	16	80	3048	RRIFLILLCLIF	242	15	75
EW	2902	IFLLVLDY	19	95	3049	LCLIFLLVLDYQGM	252	19	95
POL	2903	IGTNSVVL	16	80	3050	AKLIGTNSVLSRK	731	13	65
POL	2904	IHTAELLAA	17	85	3051	PLPIHTAELLAAACFA	711	16	80
EW	2905	IIFILLCL	16	80	3052	RRIFLILLCLLI	241	15	75
EW	2906	ILLCLIFL	20	100	3053	FLILLCLIFLLV	246	16	80
POL	2907	ILRGTSFVY	16	80	3054	ANWILRGTSFVYVPS	757	16	80
NJC	2908	ILSTLPETT	20	100	3055	NAPILSTLPETTAVR	165	19	95
EW	2909	IPPSWAF	20	100	3056	CTCIPPSWAFARF	321	8	40
NJC	2910	IRTPPAYRP	19	95	3057	GVWIRTPPAYRPNA	123	19	95
POL	2911	LAACFARSR	17	85	3058	AELLAACFARSRGA	717	16	80
POL	2912	LAFSYMDDV	18	90	3059	PHCLAFSYMDDVWLG	531	18	90
POL	2913	LAQFSAIC	19	95	3060	PFLAQFSAICSVV	512	19	95
NJC	2914	LCLGWLWGM	17	85	3061	ASKLCLGWLWGMID	19	17	85
EW	2915	LCLIFLLV	20	100	3062	ILLCLIFLLVLDY	249	19	95
X	2916	LCLRPVGA	19	95	3063	RDVLCCLRPVGAESRG	13	18	90
POL	2917	LCQVFADAT	19	95	3064	RPGLCQVFADATPTG	680	11	55
EW	2918	LDSWWTSLN	19	95	3065	POSLSWWTSLNPLG	192	17	85
NJC	2919	LOTASALYR	17	85	3066	RDLDLOTASALYREAL	28	16	80
POL	2920	LDVSAAFYH	19	95	3067	WLSLDVSAAFYHIPL	425	11	55
EW	2921	LDYQGMPLV	18	90	3068	LVLDDYQGMPLVCPPL	258	18	90
POL	2922	LEELPRLA	18	90	3069	AGPLEELPRLADEG	18	13	65
EW	2923	LFILLCLLI	16	80	3070	IIFLILLCLIFLL	244	16	80

Table XIXa

HBV DR-SUPER MOTIF

Protein	Core SEQ ID NO:	Core Sequence	Core Freq.	Core Conservancy (%)	Exemplary SEQ ID NO:	Exemplary Sequence	Position In HBV Poly-Protein	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
POL	2924	LGAKSVQHL	17	85	3071	DWLGAKSVQHLES	541	16	80
POL	2925	LGFAAPTQ	19	95	3072	VGLGFAAPTQCGY	626	19	95
POL	2926	LGFRKPMG	19	95	3073	PILGFRKPMGVGL	496	13	65
POL	2927	LGNLNVSP	19	95	3074	DNLGNLNVSPWTH	40	19	95
BW	2928	LGPLLVLQA	19	95	3075	SGRLPLLVLQAGFF	169	15	75
POL	2929	LHPAAMPHL	20	100	3076	HLPLHPAAMPHLVVG	425	9	45
BW	2930	LFLVLDD	19	95	3077	LLQFLVLVLDYQG	251	19	95
POL	2931	LKLMPARF	15	75	3078	KRLKLMPARFYFN	104	7	35
X	2932	LKPVLGCC	15	75	3079	EIRKPVVLGGGRHK	126	13	65
POL	2933	LLAQFTSAI	19	95	3080	SPFLAQFTSAICSV	511	19	95
NC	2934	LLDTASALY	17	85	3081	IRDLDTASALYREA	56	9	45
POL	2935	LLGCAANWI	16	80	3082	FWLLGCAANWILRG	749	15	75
POL	2936	LLGFAAPT	19	95	3083	IVGLLGAAPTQCG	625	18	90
BW	2937	LLGWSPOAQ	17	85	3084	HGGLLGSWSPOAQJIL	60	15	75
BW	2938	LLLCUFL	20	100	3085	LFILLLCUFLVLL	247	16	80
NC	2939	LLSFLPSDF	19	95	3086	SVLLSFLPSDFPS	41	11	55
POL	2940	LLSLGHLN	19	95	3087	TNLLSLGHLNPNK	560	15	75
POL	2941	LLSSNLSSL	18	90	3088	LTNLLSSNLSSL	404	18	90
BW	2942	LLTRILTIP	16	80	3089	GFLLTRILTIPQSL	181	16	80
BW	2943	LLVLOAGFF	19	95	3090	LGPLLVLQAGFFLLT	172	18	90
BW	2944	LLVPFQWVF	20	100	3091	WLSSLVPFQWVFGL	335	19	95
NC	2945	LLWFHISQL	18	90	3092	IRQLLWFHISQLTFG	126	13	65
POL	2946	LMPLYACIQ	19	95	3093	YPALMPLYACIQSKQ	640	11	55
POL	2947	LNLGNLNV	15	95	3094	AEDLNLGNLNVSPW	38	19	95
POL	2948	LNPNTKRW	15	75	3095	GHLPNPKTKRWGYS	567	15	75
POL	2949	LNRRVAEDL	17	85	3096	DEGLNRRVAEDLNLG	30	12	60
POL	2950	LNVSPWTH	19	95	3097	LGNLNVSPWTHKVG	43	19	95
NC	2951	LPETTVRR	19	100	3098	LSTLPETTVRRRGR	169	16	80
BW	2952	LPIFFQLWV	20	95	3099	LPLPIFFQLWVYZ	376	13	65
POL	2953	LPIHTAELL	17	85	3100	VAPLPIHTAELLAAC	709	9	45
POL	2954	LPVNRPDW	16	80	3101	FRKLPVNRPDWKC	608	15	75
POL	2955	LQFRNKP	18	90	3102	CWWLQFRNKPQSDY	312	10	50
X	2956	LRGLPVCAF	19	95	3103	HLSLRGLPVCAFSSA	52	18	90
X	2957	LRPVGAESR	18	90	3104	VLCLRPVGAESRGRP	15	18	90
NC	2958	LROALCWG	18	90	3105	HTALROALCWGELM	52	18	90
BW	2959	LRRFIHLF	15	75	3106	WMCLRRFIHLFILL	237	15	75
NC	2960	LSFLPSDF	19	95	3107	VLLSFLPSDFPSI	42	10	50
POL	2961	LSLSDVSAF	19	95	3108	LSWLSDVSAAFYHI	423	11	55
BW	2962	LSLLVPFVQ	20	100	3109	FSWLSLLVPFVQWVF	333	19	95
X	2963	LSRLGLPVC	19	95	3110	GAHLSRLGLPVCAPS	50	18	90
POL	2964	LSPELLAQF	19	95	3111	GVGLSPELLAQFSA	507	16	80
POL	2965	LSRKYSFP	17	85	3112	SWLSRKYSFPWILL	739	17	85
POL	2966	LSSNLSSL	18	90	3113	TNLLSSNLSSL	405	18	90
BW	2967	LSVNPPLGF	15	75	3114	GTNLSVNPPLGFFPD	13	14	70
POL	2968	LSWLSLDS	20	100	3115	SSNLWSLSDVSAF	409	17	85
BW	2969	LTIPOSLDS	18	90	3116	TRILTIPQSLDSWWT	186	15	75
POL	2970	LTNLLSSL	18	90	3117	LOSLTNLLSSNLSSL	401	18	90
BW	2971	LTRILTIPQ	16	80	3118	FFLLTRILTIPQSLD	182	15	75
POL	2972	LVDKNPHNT	20	100	3119	GVFLVDKNPHNTTES	372	11	55
NC	2973	LVSFGWIR	18	90	3120	LEYLVSFGWIRTPP	145	14	70

Table XIXa

HBV DR-SUPER MOTIF

Protein	Core SEQ ID NO:	Core Sequence	Core Freq.	Core Conservancy (%)	Exemplary SEQ ID NO:	Exemplary Sequence	Position In HBV Poly-Protein	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
POL	2974	LWDFSQFS	20	100	3121	ESRLWDFSQFSRGN	374	9	45
NUC	2975	LWFHISCLT	17	85	3122	ROLLWDFHISCLTIFGR		17	85
NUC	2976	LWGMIDIPY	17	85	3123	LGWLWGMIDIPYKEF	24	17	85
POL	2977	LWKAGILYK	20	100	3124	LHTLWKAGILYKRET	148	18	90
NUC	2978	LYREALESP	17	85	3125	ASALYREALESPHC	34	17	85
POL	2979	LYSHIPILG	16	80	3126	KLHLYSHIPILGFRK	489	16	80
POL	2980	MDDVVLGAK	18	90	3127	FSYMDDVVLGAKSVQ	536	18	90
POL	2981	MGVGLSPFL	16	80	3128	KIPMGVGLSPFLAQ	503	16	80
POL	2982	MPHLLVGSS	17	85	3129	PAAMPHLLVGSSGLS	430	8	40
BN	2983	MOVNSTTFH	16	80	3130	POAMOVNSTTFHQTIL	106	8	40
X	2984	MSTTDLEAY	15	75	3131	LSAMSTTDLEAYFKD	100	9	45
BN	2985	MYWYGPSLY	17	85	3132	IWMWYGPSLYNIL	369	9	45
X	2986	VCAFSSAGP	19	95	3133	GLPVCAFSSAGPCAL	57	18	90
POL	2987	VQRIVGLL	17	85	3134	DMKYCQRIVGLLGFA	618	17	85
POL	2988	VFADATPTG	19	95	3135	LCQVFADATPTGWGL	683	19	95
BN	2989	VGLSPTVWL	19	95	3136	QWVFGLSPTVWLVI	344	14	70
POL	2990	VGPLTVNEK	17	85	3137	QQYVGPLTVNEKRL	93	8	40
POL	2991	VHFASPLHV	16	80	3138	PDRVHFASPLHVAVIR	816	12	60
X	2992	VLCLRPVGA	19	95	3139	ARDVLCLRPVGAESR	12	14	70
POL	2993	VLGAKSVQIH	19	95	3140	DDWLGLGAKSVQIHLES	540	16	80
X	2994	VLHRTILGL	17	85	3141	LPKVLHRTILGLSAM	89	11	55
POL	2995	VFNLSLTN	19	95	3142	KFAVFNLSLTNLLS	395	19	95
NUC	2996	VDASKCLG	16	80	3143	CPTVQASKCLGLGLW	14	15	75
BN	2997	VRFSLSL	16	95	3144	WASVRFSLSLVPPF	328	13	65
POL	2998	VRFAPFHL	19	95	3145	CSVVRAPFHLAFLS	523	19	95
POL	2999	VSIPWTHKV	20	100	3146	NLNSIPWTHKVGINF	45	19	95
NUC	3000	VWIRTPPAY	19	95	3147	SFGVWIRTPPAYRPP	121	18	90
POL	3001	VYVPSALNP	18	90	3148	TSFYVPSALNPADD	764	16	80
BN	3002	WFHISCLTF	18	90	3149	QLLWFHISCLTFGRE	99	17	85
POL	3003	WPGVLSPTV	19	95	3150	FVQWPGVLSPTVWLS	342	19	95
BN	3004	WILRGTSFY	16	80	3151	AANWILRGTSFYVVP	756	14	70
NUC	3005	WIRTPPAYR	19	95	3152	FGWIRTPPAYRPPN	122	19	95
POL	3006	WKAGILYKR	20	100	3153	HTLWKAGILYKRETT	149	18	90
POL	3007	WLLGCAANW	16	80	3154	SFPWLLGCAANWILR	748	15	75
BN	3008	WLSLDVSA	19	95	3155	NLSWLSLDVSAAFYH	411	17	85
BN	3009	WLSLLVPPV	20	100	3156	RFSWLSLLVPPVQWF	332	20	100
POL	3010	WPKFAPNLI	19	95	3157	RVSWPKFAPNLSQSL	332	11	55
POL	3011	YMDDVWLGA	18	90	3158	AFSYMDDVWLGAHSV	535	18	90
POL	3012	YPALMPLVA	19	95	3159	OCGYPALMPLVACIQ	637	19	95
BN	3013	YOGMLPVC	18	90	3160	LLDYOGMLPVCPLUP	260	10	50
NUC	3014	YRPPNAPIL	20	100	3161	PPAYRPPNAPILSTL	129	19	95
BN	3015	YRWMCLRRF	19	95	3162	CPGYRWMCLRRFIIF	232	19	95
POL	3016	YSHIPILGF	16	80	3163	LHLYSHIPILGFRKI	490	16	80
POL	3017	YSLNRMGYV	15	75	3164	RWGYSLNRMGYVIGS	588	11	55
POL	3018	YVPSALNPA	18	90	3165	SFYVPSALNPADDP	765	16	80
BN	3019	FFCLWVYIZ	20				382		
BN	3020	MGTNLSVNP	15				12		

HBV DR-SUPER MOTIF With Binding Data

Table XIXB

Core SEQ ID NO:	Core Sequence	SEQ ID NO:	Exemplary Sequence	DR1	DR2w2h1	DR2w2h2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	DR6w19	DR7	DR8w2	DR9	Drw53
2874	FAAPFTOCG	3021	LLGFAAPFTOCGYPA													
2875	FADATPTGW	3022	QQVFADATPTGWGLA													
2876	FAPNLOSL	3023	WPKFAVFNLOSLTNL													
2877	FGRETVEY	3024	CLTFGRETVEYLVLS													
2878	FGVEPSGG	3025	RRSFGVEPSGGHID													
2879	FHISCLTFG	3026	LLWFHISCLTFGRET													
2880	FHCLLISC	3027	MLFHLCLISCSCP													
2881	FILLCLIF	3028	IFLFIILLCLIFLV													
2882	FLILLCL	3029	FIIFLILLCLIFL													
2883	FLGPLLVQ	3030	TSGFLGPLLVLOAGF													
2884	FLTRILTI	3031	AGFELLTRILTIQS													
2885	FLVLVDYQ	3032	CLIFLLVLVDYQGM													
2886	FPAAGSSG	3033	GLYFPAAGSSSGTVN													
2887	FPDHLDP	3034	LGFFPDHQLDPAFGA													
2888	FPCLAFSY	3035	RRAFPCLAFSYMDD													
2889	FRKIPMGV	3036	ILGFRKIPMGVGLSP													
2890	FRKLPVNR	3037	KQCFRKLVPNRPIDW													
2891	FSSAGPCAL	3038	VCAFSSAGPCALRFT													
2892	FSWLSLLV	3039	SVRFWSWLSLLVPFVQ													
2893	FTFSPYKA	3040	KQAFFTFSPYKAFLC													
2894	FTGLYSYTV	3041	VGNFTGLYSYTVFV													
2895	FTSACSVV	3042	LAQFTSACSVVRRRA													
2896	FVGLSPTVW	3043	QWVGLSPTVWLSV													
2897	FVLGGCRHK	3044	KVFLVGGCRHKLVLC													
2898	FVQVFWGLS	3045	LVPFVQVFWGLSPTV													
2899	FVYVPSALN	3046	GRSFVYVPSALNPAD													
2900	IDWVKCQR	3047	NRPIDWVKCQRIVGL													
2901	IFELLCL	3048	RFIIFELLCLIF													
2902	IFLVLLDY	3049	LCLIFLVLLDYQGM													
2903	IGTNSWL	3050	AKLIGTNSWLSRK													
2904	IHTAELAA	3051	PLPIHTAELAAACFA													
2905	IIFLLILL	3052	RRFIIFLLILLCL													
2906	ILLCLIFL	3053	FLFIILLCLIFLLV													
2907	ILRGTSFY	3054	ANWILRGTSFYVPS													
2908	ILSTLPETT	3055	NAPILSTLPETTWR													
2909	PIPPSSWAF	3056	CTCIPIPPSSWAFARF													
2910	IRTPPAYRP	3057	GWIRTPPAYRPPNA													
2911	LAACFARSR	3058	AELLAACFARSRGA													
2912	LAFSYMDV	3059	PHCLAFSYMDVVLG													
2913	LAQFSAIC	3060	PELLAQFSAICSVW													
2914	LCLGWLWGM	3061	ASKLCLGWLWGMID													
2915	LCLIFLLV	3062	ILLCLIFLLVLLDY													
2916	LCLRPVGA	3063	RDVCLRPVGAESRG													
2917	LQVAFADAT	3064	RPGLQVAFADATPTG													
2918	LDVWMTSLN	3065	POSLDVWMTSLNFLG													
2919	LDTSALYR	3066	RDLDTASALYREAL													
2920	LDVSAAFYH	3067	WLSLDVSAAFYHIPL													
2921	LDYQGMPLV	3068	LVLDYQGMPLVCPPL													
2922	LEEELPRLA	3069	AGPLEELPRLADEG													
2923	LFILLCL	3070	IIFLILLCLIFLL													

[illegible]

Core SEQ ID NO:	Core Sequence	SEQ ID NO:	Exemplary Sequence	DR1	DR2w201	DR2w202	DR3	DR4w4	DR4w15	DR5w11	DR6w12	DR6w19	DR7	DR8w2	DR9	DRw51
2974	LWDFSQFS	3121	ESRLWDFSQFSRGN	0.0007	0.0074	-0.0010	2.6000			-0.0004		0.0040	-0.0014	0.0029		0.0096
2975	LWFHISCLT	3122	ROLLWFIHISCLTGR	0.0002		0.0009		0.0140		0.0011			0.0061			0.0430
2976	LWGMDIPY	3123	LGLWGMGMDIPYKEF	0.0004		0.0006	0.0200	0.0280		-0.0002			0.0004			
2977	LWKAGILYK	3124	LHTLWKAGILYKRET													
2978	LYREALESP	3125	ASALYREALESPHC													
2979	LYSHPIILG	3126	KLHLYSHPIILGFRK													
2980	MDDVILGAK	3127	FSYMDVILGAKSVQ													
2981	MGVGLSPFL	3128	KIPMGVGLSPFLLAO													
2982	MPHLLVGSS	3129	PAAMPHLLVGSSGLS					0.0300								
2983	MOVMNSTTFH	3130	POAMOVNSTTFHOTL	0.0012									0.1200			
2984	MSTTDLEAY	3131	LSAMSTTDLEAYFKD													
2985	MWYWGPSLY	3132	IWMWYWGPSLYNIL													
2986	VCAFSSAGP	3133	GLPVCAFSSAGPCAL													
2987	VCOIRVGLL	3134	DMKVCOIRVGLLGA	0.0120		-0.0026		0.0030		0.2500			0.0018			0.0130
2988	VFADATPTG	3135	LCOVFADATPTGWGL	0.0020				0.9600					0.0013			
2989	VGLSPTWL	3136	QWVFGLSPTWLSVI													
2990	VGPLTVNEK	3137	QOYVGPLTVNEKRL													
2991	VHFASPLHV	3138	PDVHFASPLHVAVR	0.0510	0.0290	0.0008		0.0008	0.0054	0.0008		0.0190	0.0810	0.0035	0.2400	
2992	VLCFLRPVA	3139	APDVLCFLRPVGAESR													
2993	VLGAKSVQH	3140	DDVLGAKSVQHLES													
2994	VLHKRTLGL	3141	LPKVLHKRTLGLSAM													
2995	VPLNQLSTN	3142	KFAPVPLNQLSTNLLS	0.0180	0.0005	-0.0003		0.1300		0.0043		0.0088	-0.0003		0.0056	
2996	VOASKLCLG	3143	CPTVOASKLCLGWLW													
2997	VRESMSLL	3144	WASVRESMSLLVPF													
2998	VRAFPHOL	3145	CSVRAFPHOLCLAFS	0.1000	0.1024	0.0770	0.0032	0.0016	-0.0022	0.0008	-0.0013	0.0540	0.0590	0.0250	1.2000	0.0460
2999	VSPWTHKV	3146	NLNVSPIWTHKVGNF	0.0001		-0.0005	-0.0041	-0.0007		-0.0002			0.0005			0.0009
3000	WVIRTPPAY	3147	SFGWVIRTPPAYRPP	0.0094	0.0110	0.4300	-0.0009	0.0780	0.0630	0.0260	0.0071	0.0002	0.0240	0.2500	0.0800	0.0016
3001	VYVPSALNP	3148	TSFYVPSALNPADD													
3002	WLHISCLTF	3149	QLLWHLISCLTFGRE													
3003	WFVGLSPTV	3150	FLQWVFGVGLSPTWLS	0.4700	0.0035	0.0160	-0.0013	0.0130		0.0072	0.0021	0.0190	0.0690	0.0180	0.0410	0.0044
3004	WILRGTSFV	3151	ANWILRGTSFVYVP	0.0920	0.0240	0.0061	0.0023	0.0510	0.0250	0.0140	0.3700	0.0250	0.5800	0.2500	0.2700	
3005	WIRTPPAYR	3152	FGWVIRTPPAYRPPN													
3006	WKAGILYKR	3153	HT													

Table XXa

HBV DR-3A Motif

Protein	Core SEQ ID NO:	Core Sequence	Core Freq.	Core Conservancy (%)	Exemplary SEQ ID NO:	Exemplary Sequence	Position In Poly-Protein	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
ENV	3166	FFPDHOLDP	19	95	3181	PLGFRPHOLDPAFG	10	9	95
NC	3167	FGRETVLEY	15	75	3182	CLTFGRETVLEYLV	136	14	75
POL	3168	FGVPSGSG	15	75	3183	RRSGVPSGSGHD	241	6	75
POL	3169	FLVDKNPHN	20	100	3184	GGVFLVDKNPHNTE	360	11	100
POL	3170	IGTONSWL	16	80	3185	AKUGTDSNVLSRK	731	13	80
POL	3171	LEELPRLA	18	90	3186	AGPLEELPRLADEG	18	13	90
POL	3172	LPDKGMP	20	100	3187	TKYLPDKGMPYP	120	20	100
POL	3173	LSLDVSAF	19	95	3188	LSWLSLDVSAAFYHI	412	11	95
POL	3174	LWDFSOFS	20	100	3189	ESRLWDFSOFSRGN	374	9	100
NC	3175	LYREALESP	17	85	3190	ASALYREALESPHC	34	17	85
NC	3176	MDQPYKEF	17	85	3191	LWGMDDPYKEFGAS	27	9	85
POL	3177	VAEDNLGN	20	100	3192	NRRVAEDNLGNLNV	34	17	100
POL	3178	VFADATPTG	19	95	3193	LCOVFADATPTGWGL	683	19	95
ENV	3179	VLLDYQGML	19	95	3194	FLVLLDYQGMLPVC	256	18	95
POL	3180	YMDDVILGA	18	90	3195	AFSYMDDDVILGAKSV	535	18	90

HCV DR 3A Motif

Table XXb

Core SEQ ID NO:	Core Sequence	SEQ ID NO:	Exemplary Sequence	DR1	DR2w201	DR2w202	DR3	DR4w4	DR4w15	DR5w11	DR5w12	DR6w19	DR7	DR8W2	DR9	DRW53
3166	FFPHOLDP	3181	PLGFPQHQDPAFG													
3167	FGRETVLEY	3182	CLTFGRETVLEYVS													
3168	FGVPSGSG	3183	RRSGVPSGSGHD				0.0790									
3169	FLVDKNPHN	3184	GGVFLVDKNPHNTE													
3170	IGTONSVL	3185	AKUGTDSVLSRK													
3171	LEELPRLA	3186	AGPLEELPRLAEG				0.0022									
3172	LPLDKGKP	3187	TKYLPDKGKPYYP				-0.0017									
3173	LSLDVSAF	3188	LSWLSLDVSAFYHI													
3174	LVDFSQFS	3189	ESRLVDFSQFSRGN	0.0007	0.0074	-0.0010	2.8000		-0.0004	0.4000	-0.0014	0.0029				
3175	LYREALESP	3190	ASALYREALESPHC													
3176	MDPYKEF	3191	LWGMIDDPYKEFGAS				0.1400									
3177	VAEDNLGN	3192	NRRVAEDNLGNLNV					0.9600								
3178	VFADATPTG	3193	LQVVFADATPTGWL	0.0020			0.0170					0.0013				
3179	VLDYOGML	3194	FLVLDYOGMLPVC					2.9000				-0.0003				
3180	YMDQVVLGA	3195	AFSYMDQVVLGAQSV	0.0027		-0.0005	0.0130		0.0006							-0.0005

HBV DR-3B Motif

Table XXc

Protein	Core SEQ ID NO:	Core Sequence	Core Freq.	Core Conservancy (%)	SEQ ID NO:	Exemplary Sequence	Position In HBV Poly-Protein	Exemplary Sequence Frequency	Exemplary Sequence
X	3196	AHLSRLGLP	18	90	3202	DHGAHLSRLGLPVCA	48	18	90.00
POL	3197	FSPTYKAF	19	95	3203	AFTFSPTYKAFCKQ	655	11	55.00
POL	3198	IPWTHKVG	20	100	3204	NVSIPWTHKVGNGFTG	47	20	100.00
POL	3199	LTVNEKRRL	17	85	3205	VGPLTVNEKRRLKLI	96	12	60.00
X	3200	VGAESRRFP	19	95	3206	LPPVGAESRRFPVSG	18	7	35.00
POL	3201	VLSRKYS	18	90	3207	DNSVLSRKYSFPW	737	17	85.00

TABLE XXI. Population coverage with combined HLA Supertypes

<u>HLA-SUPERTYPES</u>	<u>PHENOTYPIC FREQUENCY</u>					
	Caucasian	North American Black	Japanese	Chinese	Hispanic	Average
<u>a. Individual Supertypes</u>						
A2	45.8	39.0	42.4	45.9	43.0	43.2
A3	37.5	42.1	45.8	52.7	43.1	44.2
B7	38.6	52.7	48.8	35.5	47.1	44.7
A1	47.1	16.1	21.8	14.7	26.3	25.2
A24	23.9	38.9	58.6	40.1	38.3	40.0
B44	43.0	21.2	42.9	39.1	39.0	37.0
B27	28.4	26.1	13.3	13.9	35.3	23.4
B62	12.6	4.8	36.5	25.4	11.1	18.1
B58	10.0	25.1	1.6	9.0	5.9	10.3
<u>b. Combined Supertypes</u>						
A2, A3, B7	83.0	86.1	87.5	88.4	86.3	86.2
A2, A3, B7, A24, B44, A1	99.5	98.1	100.0	99.5	99.4	99.3
A2, A3, B7, A24, B44, A1, B27, B62, B58	99.9	99.6	100.0	99.8	99.9	99.8

Table XXII

HBV ANALOGS

AA	Sequence	Fixed Nomen.	A1 Motif	A2 Super Motif	A3 Super Motif	A24 Motif	B7 Super Motif	1° Anchor Fixer	Analog	SEQ ID NO:
10	CILLCLIFL		N	Y	N	N	N	No	A	3208
9	RMTGGVFLV	VM2.V9	N	Y	N	N	N	1	A	3209
9	LMPFQWFLV	VM2.V9	N	Y	N	N	N	1	A	3210
9	RLTGGVFLV	VL2.V9	N	Y	N	N	N	1	A	3211
9	GLCQVADV	L2.AV9	N	Y	N	N	N	1	A	3212
9	WLLRGTSFV	IL2.V9	N	Y	N	N	N	1	A	3213
9	NLGNLNVSV	L2.IV9	N	Y	N	N	N	1	A	3214
9	YLPALNPV	VL2.AV9	N	Y	N	N	N	1	A	3215
9	GLWIRTPPV	VL2.AV9	N	Y	N	N	N	1	A	3216
9	RLSWPKFAV	VL2.V9	N	Y	N	N	N	1	A	3217
9	ILGLLGFAV	VL2.AV9	N	Y	N	N	N	1	A	3218
9	RMLTIQSV	IM2.LV9	N	Y	N	N	N	1	A	3219
9	SLDSWWTSTV	L2.LV9	N	Y	N	N	N	1	A	3220
10	FMLLCLIFL	IM2.L10	N	Y	N	Y	N	1	A	3221
10	LMLQAGFFLV	VM2.LV	N	Y	N	N	N	1	A	3222
10	SMLSPFLPLV	IM2.LV1	N	Y	N	N	N	1	A	3223
10	LMLLDYQGMV	VM2.LV	N	Y	N	N	N	1	A	3224
10	FLGLSPTWV	VL2.LV1	N	Y	N	N	N	1	A	3225
8	FPAAMPHL		N	N	N	N	N		A	3226
8	HPFAMPHL		N	N	N	N	N		A	3227
8	HPAAMPHI		N	N	N	N	N		A	3228
8	FMFSPTYK		N	N	N	N	N		A	3229
8	FVFSPTYK		N	N	N	N	N		A	3230
9	FLLTRILTV	L2.IV9	N	Y	N	N	N	1	A	3231
9	ALMPLYACV	L2.IV9	N	Y	N	N	N	1	A	3232
9	LLAQFTSAV	L2.IV9	N	Y	N	N	N	1	A	3233
9	LLPFVQWFLV	VL2.V9	N	Y	N	N	N	1	A	3234
9	FLLAQFTSV	L2.AV9	N	Y	N	N	N	1	A	3235
9	KHLYSHPV	L2.IV9	N	Y	N	N	N	1	A	3236
9	KFLYSHPI		N	Y	N	N	N	No	A	3237
9	LLSSNLWSV	L2.LV9	N	Y	N	N	N	1	A	3238
9	FLSLGIHV	L2.LV9	N	Y	N	N	N	1	A	3239
9	MMWYWGSPSV	M2.LV9	N	Y	N	N	N	1	A	3240
9	VLOAGFFLV	L2.LV9	N	Y	N	N	N	1	A	3241
9	PLPIFFCV	L2.LV9	N	Y	N	N	N	1	A	3242
9	FLPIFFCL		N	Y	N	N	N	No	A	3243
9	VLLDYQGMV	L2.LV9	N	Y	N	N	N	1	A	3244
9	YMFEDWLGA		N	Y	N	N	N	No	A	3245
9	GLLGWSPQV	L2.AV9	N	Y	N	N	N	1	A	3246
9	FPAAMPHLL		N	N	N	N	N		A	3247
9	HPFAMPHILL		N	N	N	N	N		A	3248
9	HPAAMPHLI		N	N	N	N	N		A	3249

Table XXII

HBV ANALOGS

AA	Sequence	Fixed Nomen.	A1 Motif	A2 Super Motif	A3 Super Motif	A24 Motif	B7 Super Motif	1° Anchor Fixer	Analog	SEQID NO:
9	FPVCAFSSA		N	N	N	N	Y		A	3250
9	LPFCAFSSA		N	N	N	N	Y		A	3251
9	LPVCAFSSI		N	N	N	N	Y		A	3252
9	FPALMPLYA		N	N	N	N	Y		A	3253
9	YPFLMPLYA		N	N	N	N	Y		A	3254
9	YPALMPLYI		N	N	N	N	Y		A	3255
9	FPSRGRGLL		N	N	N	N	Y		A	3256
9	DPRGRGLL		N	N	N	N	Y		A	3257
9	DPSRGRGLI		N	N	N	N	Y		A	3258
9	SMICSVVRR		N	N	Y	N	N		A	3259
9	SVICSVVRR		N	N	Y	N	N		A	3260
9	KVGNFTGLK		N	N	Y	N	N		A	3261
9	KVGNFTGLR		N	N	Y	N	N		A	3262
9	WFFSQFSR		N	N	Y	N	N		A	3263
9	SVNRPIDWK		N	N	Y	N	N		A	3264
9	TLWKAGILK		N	N	Y	N	N		A	3265
9	TLWKAGILR		N	N	Y	N	N		A	3266
9	TMWKAGILY		Y	N	Y	N	N		A	3267
9	TVWKAGILY		N	N	Y	N	N		A	3268
9	RMYLHTLWK		N	N	Y	N	N		A	3269
9	RVYLHTLWK		N	N	Y	N	N		A	3270
9	AMTFSPTYK		N	N	Y	N	N		A	3271
9	SVRRRAFPR		N	N	Y	N	N		A	3272
9	SVRRRAFPK		N	N	Y	N	N		A	3273
9	SAIXSVVRR		N	N	Y	N	N		A	3274
9	LPVXAFSSA		N	N	N	N	Y		A	3275
10	FLAQFTSAV	L2.IV10	N	Y	N	N	N	1	A	3276
10	YLFTLWKAGI		N	Y	N	N	N	No	A	3277
10	YLLTLWKAGI		N	Y	N	N	N	No	A	3278
10	LLFYQGMPLV		N	Y	N	N	N	No	A	3279
10	LLLYQGMPLV		N	Y	N	N	N	No	A	3280
10	LLVLQAGFFV	L2.LV10	N	Y	N	N	N	1	A	3281
10	ILLCLCLFLV	L2.LV10	N	Y	N	N	N	1	A	3282
10	FPFLAFSYM		N	N	N	N	Y		A	3283
10	FPHCLAFSYI		N	N	N	N	Y		A	3284
10	FPARVTGGVF		N	N	N	N	Y		A	3285
10	TPRVTGGVF		N	N	N	N	Y		A	3286
10	TPRVTGGVI		N	N	N	N	Y		A	3287
10	FPCALRFTSA		N	N	N	N	Y		A	3288
10	GPFAIRFTSA		N	N	N	N	Y		A	3289
10	GPCALRFTSI		N	N	N	N	Y		A	3290
10	FPAAMPHELLV		N	N	N	N	Y		A	3291

HBV ANALOGS

Table XXII

AA	Sequence	Fixed Nomen.	A1 Motif	A2 Super Motif	A3 Super Motif	A24 Motif	B7 Super Motif	1° Anchor Fixer	Analog	SEQ ID NO.
10	HPFAMPHLLV		N	N	N	N	Y		A	3292
10	HPAAMPHLLI		N	N	N	N	Y		A	3293
10	QMFTFSPTYK		N	N	Y	N	N		A	3294
10	QVFTFSPTYK		N	N	Y	N	N		A	3295
10	TMWKAGILYK		N	N	Y	N	N		A	3296
10	TVWKAGILYK		N	N	Y	N	N		A	3297
10	VMGGVFLVDK		N	N	Y	N	N		A	3298
10	WGGVFLVDK		N	N	Y	N	N		A	3299
10	SMLPETTVVR		N	N	Y	N	N		A	3300
10	SVLPETTVWR		N	N	Y	N	N		A	3301
10	TMPETTVRR		N	N	Y	N	N		A	3302
10	TVPETTVRR		N	N	Y	N	N		A	3303
10	HTLWKAGILK		N	N	Y	N	N		A	3304
10	HTLWKAGILR		N	N	Y	N	N		A	3305
10	HMLWKAGILY		Y	N	Y	N	N		A	3306
10	HVLWKAGILY		N	N	Y	N	N		A	3307
10	GMDNSWLSR		N	N	Y	N	N		A	3308
10	GDNSWLSR		N	N	Y	N	N		A	3309
10	GTNSWLSR		N	N	Y	N	N		A	3310
10	YMFDFVLGAK		N	N	Y	N	N		A	3311
10	MMWYWGPSLK		N	N	Y	N	N		A	3312
10	MMWYWGPSLR		N	N	Y	N	N		A	3313
9	ILLXLIFL		N	Y	N	N	N		A	3314
9	LLXLIFLL		N	Y	N	N	N		A	3315
9	LLXLIFLV		N	Y	N	N	N		A	3316
9	PLLPFFXL		N	Y	N	N	N		A	3317
9	ALMPLYAXI		N	Y	N	N	N		A	3318
9	GLXQVFADA		N	Y	N	N	N		A	3319
9	HISLTFGR		N	N	Y	N	N		A	3320
9	FVLGGXRHK		N	N	Y	N	N		A	3321
10	FILLXLIFL		N	Y	N	N	N		A	3322
10	ILLXLIFLL		N	Y	N	N	N		A	3323
10	LLXLIFLLV		N	Y	N	N	N		A	3324
10	LLPIFFXLWW		N	Y	N	N	N		A	3325
10	QLLWFHISXL		N	Y	N	N	N		A	3326
10	LLGXAANWIL		N	Y	N	N	N		A	3327
10	TSAIXSVRR		N	N	Y	N	N		A	3328
10	GYRWMXLRFF		N	N	N	N	N		A	3329
10	GPXALRFTSA		N	N	N	N	Y		A	3330
10	FPHLAFSYM		N	N	N	N	Y		A	3331
11	HMLWKAGILYK		N	N	Y	N	N		A	3332
11	HVLWKAGILYK		N	N	Y	N	N		A	3333

HBV ANALOGS

Table XXII

AA	Sequence	Fixed Nomen.	A1 Motif	A2 Super Motif	A3 Super Motif	A24 Motif	B7 Super Motif	1° Anchor Fixer	Analog	SEQID NO:
11	SMLPETTVRR		N	N	Y	N	N		A	3334
11	SVLPETTVRR		N	N	Y	N	N		A	3335
11	GMDNSWLSRK		N	N	Y	N	N		A	3336
11	GVDNSWLSRK		N	N	Y	N	N		A	3337
11	GTNSWLSRK		N	N	Y	N	N		A	3338
8	MPLSYQHI		N	N	N	N	Y		A	3339
8	LPIFFCLI		N	N	N	N	Y		A	3340
8	SPELLAQI		N	N	N	N	Y		A	3341
8	YPALMPLI		N	N	N	N	Y		A	3342
8	VPSALNPI		N	N	N	N	Y		A	3343
9	LPIFFCLWI		N	N	N	N	Y		A	3344
9	LPIHTAELI		N	N	N	N	Y		A	3345
10	VPRVQWVRGI		N	N	N	N	Y		A	3346
11	NPLGFFPDHQI		N	N	N	N	Y		A	3347
11	LPIHTAELLAI		N	N	N	N	Y		A	3348
9	FLPSYFFSA	L2.FY5.	N	Y	N	N	N	Rev3 1	A	3349
10	YUHTLWKAGV	L2.IV10	N	Y	N	N	N	1	A	3350
11	STLPETYVRR		N	N	Y	N	N		A	3351
9	YMDDWLGV	M2.AV9	N	Y	N	N	N		A	3352
9	FPIPSSWAF		N	N	N	N	N		A	3353
9	IPITSSWAF		N	N	N	N	Y		A	3354
9	IPILSSWAF		N	N	N	N	Y		A	3355
9	FPVCLAFSY		N	N	N	N	Y		A	3356
9	FPHCLAFAY		N	N	N	N	Y		A	3357
9	FPHCLAFSL		N	N	N	N	Y		A	3358
9	IPIPMWAF		N	N	N	N	Y		A	3359
9	FPHCLAFAL		N	N	N	N	Y		A	3360
10	FLPSZFFPSV		N	Y	N	N	N	No	A	3361
10	FLPSZFFPSV		N	Y	N	N	N	No	A	3362
9	IPFPSSWAF		N	Y	N	N	Y		A	3363
9	IPIFSSWAI		N	N	N	N	Y		A	3364
9	FPFCLAFSY		N	N	N	N	Y		A	3365
9	FPHCLAFSI		N	N	N	N	Y		A	3366
9	FPHCLAFSA		N	N	N	N	Y		A	3367
10	FQPSDYFFPSV		N	Y	N	N	N	Rev	A	3368
9	YLLTRILTI		N	Y	N	N	N		A	3369
9	FLYTRIITI		N	Y	N	N	N		A	3370
9	FLLTYILTI		N	Y	N	N	N		A	3371
9	FLLTRILYI		N	Y	N	N	N		A	3372
11	FLPSDFFPSVR		N	N	Y	N	N		A	3373
9	FLPSDFFPS		N	N	N	N	N		A	3374
8	FLPSDFFP		N	N	N	N	N		A	3375

HBV ANALOGS

[illegible]

Table XXIII: Immunogenicity of HBV-derived peptides

Supermotif	Peptide	Sequence	SEQ ID NO:	Protein	XRN	Immunogenicity			overall ¹
						primary	transgenic	patients	
A2 supermotif	924.07	FLPSDFPSV	3492	HBV core 18	5	10/10	6/6	25/32 ^a	+
	1069.06	LLVPFVQWFV	3493	HBV env 338	5	3/4	6/9		+
	1147.13	FLLAQFTSAI	3494	HBV pol 513	5		0/3		unk
	1090.77	YMDDVVLGV	3495	HBV pol 538	5		9/9		+
	777.03	FLLTRILTI	3496	HBV env 183	4			14/23 ^a	+
	927.15	ALMPYACI	3497	HBV pol 642	4	10/12	3/5	2/15 ^a	+
	1013.01	WLSLLVPFV	3498	HBV env 335	4	2/6	5/9	23/29 ^a	+
	1069.05	LLAQFTSAI	3499	HBV pol 504	4	0/4	0/5		unk
	1132.01	LVPFVQWFV	3500	HBV env 339	4	0/3	0/4		unk
	1147.14	VLLDYQGMLPV	3501	HBV env 259	4	4/4	6/6		+
	927.41	LLSSNLSWL	3502	HBV pol 992	3	0/4	0/3		unk
	927.42	NLSWLSLDV	3503	HBV pol 411	3		2/8		+
	927.46	KLHLYSHPI	3504	HBV pol 489	3	0/4	4/6		+
	1069.07	FLLAQFTSA	3505	HBV pol 503	3	1/2	0/3		+
	1168.02	GLSRYVARL	3506	HBV pol 455	3			9/13 ^a	+
A2 supermotif	927.11	FLLSLGHL	3507	HBV pol 562	2	15/22	12/13	9/15 ^a	+
	927.47	HLYSHPIIL	3508	HBV pol 1076	2		10/14		+
	1039.03	MMWYWGFSL	3509	HBV env 360	2	3/4	0/4		+
	1069.12	YLHTLWKAGV	3510	HBV pol 147	2	2/4			+
	1137.02	LLDYQGMLPV	3511	HBV env 260	2	1/2	0/4		+
	1142.07	GLLGWSPQA	3512	HBV env 62	2	3/4	5/6		+
	1.0573	ILRGTSFVVV	3513	HBV pol 773	1			3/7 ^b	+
	1013.14	VLQAGFFLL	3514	HBV env 177	1	0/4	5/12		+
	1069.10	LLPIFFCLWV	3515	HBV env 378	1	3/3	0/4	2/5 ^c	+
	1069.13	PLLPIFFCL	3516	HBV env 377	1	0/4	7/12		+
	1090.06	LLVLQAGFFL	3517	HBV env 175	1	1/5	0/4		+
	1090.12	YLVSGVWI	3518	HBV nuc 118	1	9/9			+
	1.0518	GLSPTVWLSV	3519	HBV env 338	1			3/9 ^c	+
	1090.14	YMDDVVLGA	3520	HBV pol 538	1	2/7	2/5	2/7 ^b	+
A3 supermotif	1147.16	HTLWKAGILYK	3521	HBV POL 149	5	0/6	3/3	1/22	+
	1083.01	STLPETTIVRR	3522	HBV core 141	4	3/5	6/6	8/32	+
	1150.51	GSTHVSWPK	3523	HBV pol 398	4		3/6		+
	1.0219	FVLGGCRHK	3524	HBV adr "X" 1550	3	0/4			unk
	1069.16	NVSIPTWTHK	3525	HBV pol 47	3	0/8	0/3	1/21	+

A3 supermotif	1069.20	LVVDFSQFSR	3526	HBV pol 388	3	0/4	6/6	1/22	+
	1090.10	QAFTFSPTYK	3527	HBV pol 665	3	3/6	0/3	3/21	+
	1090.11	SAICSVVRR	3528	HBV pol 531	3	1/4		2/22	+
	1069.15	TLWKAGILYK	3529	HBV pol 150	2	3/8	0/3	5/28	+
	1142.05	KVGNFTGLY	3530	HBV adr POL 629	2		0/3	2/22	+
B7 supermotif	1147.05	FPCHLAFSYM	3531	HBV POL 530	5	1/3		0/12	+
	988.05	LPSDFFPSV	3532	HBV core 19-27	4			2/16	+
	1145.04	IPISSWAF	3533	HBV ENV 313	4	0/4		1/12	+
	1147.02	HPAAMPPLL	3534	HBV POL 429	4	0/5		0/12	unk
	1147.06	LPVCAFSSA	3535	HBV X 58	4	1/4			+
	1147.08	YPALMPLYA	3536	HBV POL 640	4			0/12	unk
	1145.08	FPCHLAFSYM	3537	HBV POL 541	3	0/4			unk
B7 supermotif	1147.04	TPARVTGGVF	3538	HBV POL 354	2			2/12	+

Immunogenicity evaluation derived from primary cultures, acute patients (a-Bertoni et al, J Clin Invest 100:503, b-Rehermann et al., J. Clin. Invest 97:1655, c-Nayersina et al., J Immunol 150:4659) or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems. Unk=unknown

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays

Radiolabeled peptide				SEQ ID NO:
Species	Antigen	Allele	Cell line	
Human	A1	A*0101	Steinlin	YTA VVPLVY
	A2	A*0201	JY	FLPSDYFPSV
	A2	A*0202	P815 (transfected)	FLPSDYFPSV
	A2	A*0203	FUN	FLPSDYFPSV
	A2	A*0206	CLA	FLPSDYFPSV
	A2	A*0207	721.221 (transfected)	FLPSDYFPSV
	A3		GM3107	KVFPYALINK
	A11		BVR	KVFPYALINK
	A24	A*2402	KAS116	AYIDNYNKF
	A31	A*3101	SPACH	KVFPYALINK
	A33	A*3301	LWAGS	KVFPYALINK
	A28/68	A*6801	CIR	STLPETYVVR
	A28/68	A*6802	AMAI	FTQAGYPAL
	B7	B*0702	GM3107	APRTL VYLL
	B8	B*0801	Steinlin	FLKDYQLL
	B27	B*2705	LG2	FRYNGLIHR
	B35	B*3501	CIR, BVR	FPFKYAAAF
	B35	B*3502	TISI	FPFKYAAAF
	B35	B*3503	EHM	FPFKYAAAF
	B44	B*4403	PITOUT	AEMGKYSFY
	B51		KAS116	FPFKYAAAF
	B53	B*5301	AMAI	FPFKYAAAF
	B54	B*5401	KT3	FPFKYAAAF
	Cw4	Cw*0401	CIR	QYDDAVYKL
	Cw6	Cw*0602	721.221 transfected	YRHDGGNVL
	Cw7	Cw*0702	721.221 transfected	YRHDGGNVL
Mouse	D ^b		EL4	SGPSNTYPEI
	K ^b		EL4	RGYVFQGL
	D ^d		P815	RGPYRAFVTI
	K ^d		P815	KFNPMKTYI
	L ^d		P815	IPQSLDSYWTSI

B. Class II binding assays

Radiolabeled peptide					SEQ ID NO:
Species	Antigen	Allele	Cell line	Source	
Human	DR1	DRB1*0101	LG2	HA Y307-319	YPKYVVKQNTLKLAT
	DR2	DRB1*1501	L466.1	MBP 88-102Y	VVHFFKNIVTPRTPPY
	DR2	DRB1*1601	L242.5	non-natural (760.16)	YAAFAAAKTAATAFA
	DR3	DRB1*0301	MAT	MT 65kD Y3-13	YKTIAFDEEARR
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFIGITE
	DR9	DRB1*0901	HID	Tet. tox. 830-843	QYIKANSKFIGITE
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFIGITE
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EALJHQLKINPYVLS
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFIGITE
	DR51	DRB5*0101	GM3107 or L416.3	Tet. tox. 830-843	QYIKANAKFIGITE
	DR51	DRB5*0201	L255.1	HA 307-319	PKYVVKQNTLKLAT
	DR52	DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNRDIL
	DR53	DRB4*0101	L257.6	non-natural (717.01)	YARFQSQTTLKQKT
	DQ3.1	QA1*0301/DQB1*0301	PF	non-natural (ROIV)	AHAHAHAHAHAHAHA
Mouse	IA ^b		DB27.4	non-natural (ROIV)	AHAHAHAHAHAHAHA
	IA ^d		A20	non-natural (ROIV)	AHAHAHAHAHAHAHA
	IA ^k		CH-12	HEL 46-61	YNTDGSTDYGILQNSR
	IA ^s		LS102.9	non-natural (ROIV)	AHAHAHAHAHAHAHA
	IA ^u		9I.7	non-natural (ROIV)	AHAHAHAHAHAHAHA
	IE ^d		A20	Lambda repressor 12-26	YLEDARRKKAIYEKKK
	IE ^k		CH-12	Lambda repressor 12-26	YLEDARRKKAIYEKKK

Table XXV. Monoclonal antibodies used in MHC purifi

Monoclonal antibody	Specificity
W6/32	HLA-class I
B123.2	HLA-B and C
IVD12	HLA-DQ
LB3.1	HLA-DR
M1/42	H-2 class I
28-14-8S	H-2 D ^b and L ^d
34-5-8S	H-2 D ^d
B8-24-3	H-2 K ^b
SF1-1.1.1	H-2 K ^d
Y-3	H-2 K ^b
10.3.6	H-2 IA ^k
14.4.4	H-2 IE ^d , IE ^k
MKD6	H-2 IA ^d
Y3JP	H-2 IA ^b , IA ^s , IA ^u

Table XXVI: in vitro binding of conserved HBV-derived peptides to HLA-A2-supertype alleles.

Peptide	AA	Molecule	1st Pos	Sequence	SEQ ID NO:	Consv.	A2-supertype binding capacity (IC50 nM)						Alleles bound ²
							A*0201	A*0202	A*0203	A*0206	A*6802		
924.07	10	Core	18	FLPSDFPVS	3492	95	2.5	2.1	6.0	3.0	36	5	
1069.06	10	ENV	349	LLVPFQWVFV	3493	95	7.5	11	5.9	13	286	5	
1147.13	10	POL	524	FLLAQFTSAI	3494	95	24	134	1.4	34	455	5	
1013.0102	9	ENV	346	WLSLLVPFV	3498	100	4.6	113	1.4	10	1290	4	
777.03	9	ENV	183	FLTLRLTI	3496	80	9.8	100	1.3	19	3	4	
927.15	9	POL	653	ALMPYACI	3497	95	10	126	3.0	160	851	4	
1069.05	9	POL	525	LLAQFTSAI	3499	95	50	16	3.0	1538	51	4	
1132.01	9	ENV	350	LVPFQWVFV	3500	95	119	287	2083	463	14	4	
1147.14	11	ENV	259	VLLDYQGMLPV	3501	90	8.6	20	2.0	13	2353	4	
1090.77	9	POL	538 (a)	YMDDVVILGV	3495	90	5.1	90	6.7	71	1905	4	
1069.071	9	POL	524	FLLAQFTSA	3505	95	6.0	1654	9.1	39	870	3	
927.46	9	POL	500	KLHLYSHPI	3504	95	72	126	3.7	627	26667	3	
927.42	9	POL	422	NLSWLSLDV	3503	90	77	843	16	2313	404	3	
1168.02	9	POL	455	GLSRVVARL	3506	90	79	391	18	12333	-	3	
927.41	9	POL	418	LLSSNLWL	3502	90	455	55	2.6	1370	4000	3	
1039.031	9	ENV	360	MMWYWGPSL	3509	85	5.6	5375	833	112	3636	2	
927.11	9	POL	573	FLLSLGHL	3507	95	7.7	4300	1000	34	11429	2	
1142.07	9	ENV	73	GILGWSPQA	3512	85	13	14333	286	1429	-	2	
927.47	9	POL	502	HLVSHPIIL	3508	80	23	14333	11	2176	755	2	
1137.02	10	ENV	271	LLDYQGMLPV	3511	90	51	-	500	552	-	2	
1069.09	9	ENV	270	VLLDYQGML	3573	95	114	-	476	4111	-	2	
1069.14	10	NUC	168	ILSTLPETTV	3574	100	238	506	130	1194	5970	2	
1069.11	10	POL	147	YLHTLWKAGI	3575	100	313	8600	18	4000	1250	2	
1142.01	9	NUC	129	LLWFHISCL	3576	90	385	21500	238	1194	4082	2	
1090.12	9	NUC	147	YLVSGVWI	3518	90	13	-	-	-	-	1	
1.0518	10	ENV	359	GLSPTVWLSV	3519	75	18	-	-	-	-	1	
1013.1402	9	ENV	177	VLQAGFELL	3514	95	33	2389	3704	1947	6349	1	
1069.13	9	ENV	388	PLPIFFCL	3516	100	77	-	5556	3364	8511	1	
1069.10	10	ENV	389	LLPIFFCLVW	3515	100	156	5375	667	5000	-	1	
1090.06	10	ENV	175	LLVLQAGFEL	3517	90	161	1162	2222	2467	3636	1	
1.0895	10	ENV	248	FILLCLIFL	3577	80	179	-	-	-	-	1	
927.24	9	POL	770	WLRTGSFV	3578	80	185	-	4167	-	-	1	
1090.14	9	POL	538	YMDDVVILGA	3520	90	200	-	-	-	-	1	
3.0205	10	ENV	171	FLGPLLVQA	3579	75	263	-	-	-	-	1	
1069.08	10	ENV	260	ILLCLIFLL	3580	100	263	-	-	2846	26667	1	
1.0573	10	POL	773	ILRTGSFVYV	3581	80	313	-	-	-	-	1	

1. Frequency of entire sequence amongst isolates scanned.

2. Number of supertype alleles bound. Peptides binding 3 or more alleles are considered degenerate.

3. A dash (-) indicates IC50

Table XXVII: in vitro binding of conserved HBV-derived peptides to HLA-A3-supertype alleles.

Peptide	AA	Molecule	1st Pos	Sequence	SEQ ID NO:	Consv.	A3-supertype binding capacity (IC50 nM)							Alleles	
							A*03	A*11	A*3101	A*3301	A*6801	bound	bound		
26.0535	11	X NUC FUS	299	GVWIRTPAYR	3582	95	58	35	3.0	40	12	5			
1147.16	11	pol	149	HTLWKAGILYK	3583	100	20	14	486	403	42	5			
26.0539	11	POL	376	RLVVDFOFSR	3584	95	39	2.0	7.0	24	1.0	5			
26.0149	9	X	69	CALRFTSAR	3585	85	3235	261	12	3.6	11	4			
1.0993	9	X	130	KVFLGGCR	3586	75	262	73	30	408	2667	4			
26.0153	9	X	64	SSAGPCALR	3587	90	1375	43	55	181	11	4			
1083.01	11	Core	141	STLPETTVRR	3588	95	733	4.0	180	181	26	4			
20.0130	9	pol	655	AFTFSPTYK	3589	95	42	150	3103	13182	296	3			
26.0008	8	POL	656	FTFSPTYK	3590	95	193	136	1286	1000	73	3			
1.0219	9	X	1550	FVLGGCRHK	3591	80	169	316	1500	744	103	3			
1069.20	10	POL	388	LVVDFQFSR	3592	100	6875	17	692	126	16	3			
1069.16	9	POL	47	NVSIPTWTHK	3593	100	134	105	3	2900	250	3			
1090.10	10	POL	665	QAFTFSPTYK	3594	95	244	11	18000	5088	6.7	3			
1090.11	9	POL	531	SAICSVVRR	3595	95	1897	29	1200	446	21	3			
20.0131	9	pol	524	SVVRRAPPH	3596	95	100	10	621	-	500	3			
26.0545	11	X NUC FUS	318	TLPETTVRRR	3597	95	22000	375	2951	408	13	3			
26.0023	8	X NUC FUS	296	VSGVWIR	3598	90	2750	207	240	1074	222	3			
1142.05	9	POL	55	KVGNFTGLY	3599	95	52	353	-	-	-	2			
1142.06	9	POL	623	PVNRPIDWK	3600	85	355	43	-	-	8889	2			
1.0975	9	POL	106	RLKLMPAR	3601	75	116	-	5.8	592	-	2			
1.0562	10	POL	576	SLGHLNPNK	3602	75	55	77	-	-	-	2			
1069.21	10	NUC	170	STLPETTVR	3603	95	15714	100	2250	1208	320	2			
1069.22	10	NUC	171	TLPETTVRR	3604	95	15714	261	-	2417	182	2			
1069.15	10	POL	150	TLWKAGILYK	3605	100	2.1	17	3529	29000	615	2			
1.0215	9	X	105	TTDLAAYFK	3606	75	18333	6.5	-	24167	471	2			
1069.17	10	POL	369	VTGGVFLVDK	3607	100	282	65	-	-	3636	2			
1069.19	9	POL	389	VVDFQFSR	3608	100	7333	80	13846	1706	242	2			
26.0026	8	POL	168	ASFCGSPY	3609	100	239	26	-	-	20000	2			
26.0549	11	ENV	389	LLPIFFCLWVY	3610	100	478	10000	2609	644	82	2			
26.0550	11	POL	528	RAFPCLAFSY	3611	95	92	15	667	26364	2667	2			
1090.04	10	POL	746	GTDNSVLSR	3612	90	11000	143	6000	15263	10000	1			
1069.04	10	POL	149	HTLWKAGILY	3613	100	250	7500	-	8529	6667	1			
1.0205	9	POL	771	ILRGTSFVY	3614	80	250	-	-	-	-	1			
1090.08	9	NUC	148	LVSGVWIR	3615	90	3929	500	-	-	-	1			
1039.01	10	ENV	360	MMWYWGPSLY	3616	85	220	7500	-	-	26667	1			
1.0584	10	X	104	STTDLEAYFK	3617	75	1667	2.2	-	-	-	1			
1147.17	11	pol	735	GTDNSVLSRK	3618	90	786	11	-	-	-	1			
1147.18	11	pol	357	RVGGVFLVDK	3619	100	578	207	-	-	-	1			
1099.03	9	POL	150	TLWKAGILY	3620	100	85	7500	-	-	-	1			
1090.15	10	POL	549	YMDVVVLGAK	3621	90	333	1395	-	-	-	1			
26.0024	8	POL	50	VSIPTWTHK	3622	100	846	353	5806	22308	20000	1			

1. Frequency of entire sequence amongst isolates scanned.

2. Number of superpeptide alleles bound. Peptides binding 3 or more alleles are considered degenerate.

3. A dash (-) indicates IC50

Table XXVIII: in vitro binding of conserved HBV-derived peptides to HLA-B7 supertype alleles.

Peptide	AA	Molecule	1st Pos	Sequence	SEQ ID NO:	Consv.	B7-supertype binding capacity (IC50 nM)						Alleles	
							B*0702	B*3501	B*5101	B*5301	B*5401	bound ²		
1147.05	10	POL	541	FPHCLAFSYM	3623	95	56	33	61	118	208	5		
1145.04	9	ENV	324	IPIPSSWAF	3624	100	42	2.6	2.3	12	2941	4		
1147.02	9	POL	440	HPAAMPHLL	3625	100	56	267	500	186	833	4		
1147.06	9	X	58	LPVCAFSSA	3626	95	115	101	500	10333	0.53	4		
1147.08	9	POL	651	YPALMPLYA	3627	95	306	150	162	664	0.63	4		
988.05	9	CORE	19	LPSDFPVS	3628	95	1774	343	9.0	120	4.8	4		
1145.08	9	POL	541	FPHCLAFSY	3629	95	3	14	83	17	503	3		
19.0014	8	POL	640	YPALMPLY	3630	190	13750	28	13	207	1786	3		
26.0570	11	pol	640	YPALMPLYACI	3631	95	1375	-	117	291	143	3		
1147.04	10	POL	365	TPARVTGGVF	3632	90	17	72	-	939	16667	2		
15.0034	9	ENV	390	LPIFFCLWV	3633	100	-	-	57	2325	53	2		
20.0140	9	POL	723	LPIHTAELL	3634	85	1375	114	1058	30	20000	2		
19.0006	8	ENV	340	VPFVQWVF	3635	95	5500	-	0.29	-	91	2		
19.0007	8	ENV	379	LPIFFCLW	3636	100	-	-	153	66	2857	2		
19.0010	8	POL	1	MPLSYQHF	3637	100	-	742	458	251	526	2		
19.0011	8	POL	429	HPAAMPHL	3638	100	85	18000	18	2514	625	2		
19.0012	8	POL	511	SPFLAQF	3639	95	10	8000	306	10333	1075	2		
26.0566	11	pol	511	SPFLAQFSA	3640	95	67	-	-	-	0.83	2		
1147.01	9	POL	789	DPSRGRGL	3641	90	458	-	-	-	-	1		
16.0182	10	X	67	GPCALRFTA	3642	90	61	-	-	-	2857	1		
20.0273	10	POL	440	HPAAMPHLLV	3643	85	344	3600	705	664	588	1		
15.0030	9	ENV	191	IPQLSDSWV	3644	90	-	-	27500	62	-	1		
15.0210	10	POL	123	LPLDKGKPY	3645	100	-	248	27500	-	-	1		
16.0006	9	ENV	25	FPDQLDPA	3646	90	-	8000	-	-	12	1		
16.0177	10	ENV	324	IPIPSSWAF	3647	80	4231	3000	-	6643	22	1		
16.0180	10	POL	644	APFTQCGYPA	3648	95	1897	-	-	-	7.1	1		
16.0181	10	POL	723	LPIHTAELLA	3649	85	3056	6545	-	5813	30	1		
19.0003	8	ENV	173	GPLLVLQA	3650	95	18333	-	500	-	1538	1		
19.0005	8	ENV	313	IPIPSSWA	3651	100	13750	18000	2895	-	167	1		
19.0009	8	NUC	133	RPPNAPIL	3652	100	724	-	196	-	-	1		
19.0015	8	POL	659	SPTYKAF	3653	95	14	-	2895	-	-	1		
19.0016	8	POL	769	VPSALNPA	3654	90	5000	-	786	-	10	1		
26.0554	11	pol	633	APFTQCGYPAL	3655	95	24	7200	13750	-	1075	1		
26.0559	11	pol	712	LPIHTAELLA	3656	85	611	2667	-	775	3.6	1		
26.0561	11	pol	774	NPADDPGRGL	3657	90	458	-	-	-	-	1		
26.0564	11	Core	133	RPPNAPILSTL	3658	100	42	-	3056	-	-	1		
26.0567	11	Core	49	SPHTALRQAI	3659	100	9.5	-	13750	18600	-	1		
26.0568	11	pol	354	TPARVTGGVFL	3660	90	58	-	-	18600	20000	1		

1. Frequency of entire sequence amongst isolates scanned.

2. Number of supertype alleles bound. Peptides binding 3 or more alleles are considered degenerate.

3. A dash (-) indicates IC50

Table XXIX: HBV derived A1- and A24-motif containing peptides**a. A1-motif peptides**

Peptide	Molecule	Position	Sequence	SEQ ID NO:	Conserv.	HLA-A*0101 binding (IC50 nM)
1069.01	Core	59	LLDTASALY	3661	75	2.1
1.0519	Core	419	DLLDTASALY	3662	75	2.3
1069.02	pol	427	SLDVSAAFY	3663	95	4.8
2.0239		1000	LSLDVSAAFY	3664	95	6.0
2.0126		1521	MSTTDLEAY	3665	75	29
1039.06	ENV	359	WMMWYWGPSLY	3666	85	78
1090.14	pol	538	YMDDVVLGA	3667	90	96
1090.09	pol	808	PTTGRTSLY	3668	85	119
1069.03	pol	124	PLDKGIKPY	3669	100	147
1069.08	env	249	ILLCLIFLL	3670	100	192
1069.04	pol	149	HTLWKAGILY	3671	100	381
1039.01		360	MMWYWGPSLY	3672	85	309
1.0774	Core	416	WLWGMDIDPY	3673	75	309
20.0254	pol	631	FAAPFTQCGY	3674	95	368
1.0166	pol	629	KVGNTGLY	3675	95	368

A dash indicates IC50 nM

b. A24 -motif peptides

Peptide	Molecule	Position	Sequence	SEQ ID NO:	Conserv.	HLA-A*2402 binding (IC50 nM)
20.0271	POL	392	SWPKFAVPNL	3676	95	2.1
1069.23	POL	745	KYTSPFWLL	3677	85	2.3
2.0181	POL	492	LYSHPIILGF	3678	80	11
20.0269	ENV	236	RWMCLRRFI	3679	95	11
20.0136	ENV	334	SWLSLLVPF	3680	100	31
20.0137	ENV	197	SWWTSLNFL	3681	95	32
20.0135	ENV	236	RWMCLRRFI	3682	95	169
20.0139	POL	167	SFCGSPYSW	3683	100	169
2.0173	POL	4	SYQHFRKLLL	3684	75	182
2.0060		1224	GYPALMPY	3685	95	245
13.0129	NUC	117	EYLVSGVWI	3686	90	353
1090.02	core	131	AYRPPNAPI	3687	90	387
13.0073	NUC	102	WFHISCLTF	3688	80	400
20.0138	POL	51	PWTHKVGNF	3689	100	414

A dash indicates IC50 nM

Table XXXa: Immunogenicity of HBV-derived A2-supermotif cross-reactive peptides

Peptide	Sequence	SEQ ID NO:	Protein	XRN	Immunogenicity		
					primary	transgenic	patients overall ¹
924.07	FLPSDFPSV	3690	HBV core 18	5	10/10	6/6	25/32 ^a
1069.06	LLVPFVQWFV	3691	HBV env 338	5	3/4	6/9	+
1147.13	FLLAQFTSAI	3692	HBV pol 513	5		0/3	-
1090.77	YMDDVVLGV	3693	HBV pol 538	5		9/9	+
777.03	FLLTRILTI	3694	HBV env 183	4			14/23 ^a
927.15	ALMPLYACI	3695	HBV pol 642	4	10/12	3/5	2/15 ^a
1013.01	WLSLLVPFV	3696	HBV env 335	4	2/6	5/9	23/29 ^a
1069.05	LLAQFTSAI	3697	HBV pol 504	4	0/4	0/5	-
1132.01	LVFPVQWFV	3698	HBV env 339	4	0/3	0/4	-
1147.14	VLLDYQGMLPV	3699	HBV env 259	4	4/4	6/6	+
927.41	LLSSNLSWL	3700	HBV pol 992	3	0/4	0/3	-
927.42	NLSWLSLDV	3701	HBV pol 411	3		2/8	+
927.46	KLHLYSHPI	3702	HBV pol 489	3	0/4	4/6	+
1069.07	FLLAQFTSA	3703	HBV pol 503	3	1/2	0/3	+
1168.02	GLSRYVARL	3704	HBV pol 455	3			9/13 ^a

Immunogenicity evaluation derived from primary cultures, acute patients (a-Bertoni et al, J Clin Invest 100:503, b-Rehermann et al, J. Clin. Invest 97:1655, c- Nayersina et al., J Immunol 150:4659) or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems.

Table XXXb: Immunogenicity of non-crossreactive HBV A2-supermotif peptides

Peptide	Sequence	SEQ ID NO:	Protein	XRN	Immunogenicity		
					primary	transgenic	patients overall ¹
927.11	FLLSLGIHL	3705	HBV pol 562	2	15/22	12/13	9/15 ^a
927.47	HL YSHPIIL	3706	HBV pol 1076	2		10/14	+
1039.03	MMWYWGPSL	3707	HBV env 360	2	3/4	0/4	+
1069.12	YLHTLWKAGV	3708	HBV pol 147	2	2/4		+
1137.02	LLDYQGMLPV	3709	HBV env 260	2	1/2	0/4	+
1142.07	GLLGWSPQA	3710	HBV env 62	2	3/4	5/6	+
1.0573	ILRGTSFVYV	3711	HBV pol 773	1			3/7 ^b
1013.14	VLQAGFFLL	3712	HBV env 177	1	0/4	5/12	+
1069.10	LLPIFFCLWV	3713	HBV env 378	1	3/3	0/4	2/5 ^c
1069.13	PLLPIFFCL	3714	HBV env 377	1	0/4	7/12	+
1090.06	LLVLQAGFFL	3715	HBV env 175	1	1/5	0/4	+
1090.12	YLVSGVWI	3716	HBV nuc 118	1	9/9		+
1.0518	GLSPTVWLSV	3717	HBV env 338	1			3/9 ^c
1090.14	YMDDVVLGA	3718	HBV pol 538	1	2/7	2/5	2/7 ^b

Immunogenicity evaluation derived from primary cultures, acute patients (a-Bertoni et al, J Clin Invest 100:503, b- Rehmann et al., J. Clin. Invest 97:1655, c- Nayersina et al., J Immunol 150:4659) or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems.

Table XXXc: Cross-recognition of HBV pol 538 and a Lamivudine induced pol 538 variant by CTL induced with a pol 538 analog^a.

Stimulating peptide	Day 6 CTL response (Δ LU)	
	HBV pol 538 (YMDDVVLGA) ^b	HBV pol 538 mutant (YVDDVVLGA)
HBV pol 538	27.8	54.2
HBV pol 538 mutant	35.3	27.9

a. CTLs were induced using the 1090.77 analog of HBV pol 538 (peptide 1090.14). 1090.77 was encoded in the DNA minigene pEP2.AOS.

b. Values shown represent the geometric mean of Δ LU from 2 independent cultures. Peptides loaded onto target cells were 1090.14 (HBV pol 538) or 1353.02 (a Lamivudine induced mutant of pol 538).

Table XXXIa: Immunogenicity of HBV-derived A3-supermotif cross-reactive peptides

Peptide	Sequence	SEQ ID NO:	Protein	XRN	Immunogenicity		
					primary	transgenic	patients overall ¹
1147.16	HTLWKAGILYK	3719	HBV POL 149	5	0/6	3/3	1/22 +
1083.01	STLPETTVRR	3720	HBV core 141	4	3/5	6/6	8/32 +
1150.51	GSTHVSQPK	3721	HBV pol 398	4		3/6	+ +
10219	FVLGGCRHK	3722	HBV adr "X" 1550	3	0/4		-
1069.16	NVSIPWTHK	3723	HBV pol 47	3	0/8	0/3	1/21 +
1069.20	LVVDFSQFSR	3724	HBV pol 388	3	0/4	6/6	1/22 +
1090.10	QAFTFSPTYK	3725	HBV pol 665	3	3/6	0/3	3/21 +
1090.11	SAICSVVRR	3726	HBV pol 531	3	1/4		2/22 +

1. Immunogenicity evaluation derived from primary cultures, Bertoni et al, J Clin Invest 100:503 or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems. A negative assessment (-) indicates that no responders when examined.

Table XXXIb: Immunogenicity of non-crossreactive HBV A3-supermotif peptides

Peptide	Sequence	SEQ ID NO:	Protein	XRN	Immunogenicity		
					primary	transgenic	patients overall ¹
1069.15	TLWKAGILYK	3727	HBV pol 150	2	3/8	0/3	5/28 +
1142.05	KVGNFTGLY	3728	HBV adr POL 629	2		0/3	2/22 +

1. Immunogenicity evaluation derived from primary cultures, Bertoni et al, J Clin Invest 100:503 or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems. A negative assessment (-) indicates that no responders when examined.

Table XXXIIa: Immunogenicity of HBV B7-supermotif cross-reactive peptides

Peptide	Sequence	SEQ ID NO:	Protein	XRN	Immunogenicity		
					primary	transgenic	patients overall ¹
1147.05	FPCHLAFSYM	3729	HBV POL 530	5	1/3	.	0/12 +
988.05	LPSDFPSV	3730	HBV core 19-27	4			2/16 +
1145.04	IPISSWAF	3731	HBV ENV 313	4	0/4		1/12 +
1147.02	HPAAMPPLL	3732	HBV POL 429	4	0/5		0/12 -
1147.06	LPVCAFSSA	3733	HBV X 58	4	1/4		0/12 +
1147.08	YPALMPLYA	3734	HBV POL 640	4			0/12 -
1145.08	FPCHLAFSY	3735	HBV POL 541	3	0/4		0/12 -

1. Immunogenicity evaluation derived from primary cultures, Bertoni et al, J Clin Invest 100:503 or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems. A negative assessment (-) indicates that no responders when examined.

Table XXXIIb: Immunogenicity of non-crossreactive HBV B7-supermotif peptides

Peptide	Sequence	SEQ ID NO:	Protein	XRN	Immunogenicity		
					primary	transgenic	patients overall ¹
1147.04	TPARVTGGVF	3736	HBV POL 354	2			2/12 +

1. Immunogenicity evaluation derived from primary cultures, Bertoni et al, J Clin Invest 100:503 or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems. A negative assessment (-) indicates that no responders when examined.

Table XXXIII. Candidate HBV-derived HTL epitopes

Selection criteria	Peptide	Mol	1st Pos	Conservancy		Sequence	SEQ ID NO:
				Core	Total		
DR-supermotif	F107.01	ENV	249	100	95	ILLCLIFLLVLLDY	3737
	F107.02	ENV	252	95	95	LCLIFLLVLLDYQGM	3738
	1280.17	ENV	258	90	90	LVLLDYQGMLPVCPL	3739
	1186.22	ENV	332	100	100	RFSWLSLLVPFVQWF	3740
	1186.15	ENV	339	95	95	LVPFVQWFVGLSPTV	3741
	1186.06	ENV	342	95	95	FVQWFVGLSPTVWLS	3742
	1186.03	NUC	19	85	85	ASKLCLGWLWGMID	3743
	1186.12	NUC	24	85	85	LGWLWGMIDPYKEF	3744
	857.02	NUC	50		90	PHHTALRQAILCWGELMTLA	3745
	1186.23	NUC	98	85	85	RQLLWFHISCLTFGR	3746
	27.0279	NUC	117		90	EYLVSFVWIRTPPA	3747
	27.0280	NUC	123	95	95	GVWIRTPPAYRPPNA	3748
	1186.20	NUC	129	100	95	PPAYRPPNAPILSTL	3749
	1186.16	NUC	136	100	95	NAPILSTLPETTVVR	3750
	1186.01	POL	38	95	95	AEDNLGNLNVSIW	3751
	1186.17	POL	45	100	95	NLNVSIWTHKVGNF	3752
	27.0281	POL	145	100	100	RHYLHTLWKAGILYK	3753
	1280.13	POL	406	95	95	KFAVPNLQSLTNLLS	3754
	27.0283	POL	409		85	VPNLQSLTNLLSSNL	3755
	F107.03	POL	412	90	90	LQSLTNLLSSNLSWL	3756
	1186.28	POL	416	90	90	TNLLSSNLSWLSLDV	3757
	1186.27	POL	420	100	85	SSNLSWLSLDVSAAF	3758
	F107.04	POL	523	95	95	PFLAQFTSAICSVV	3759
	1186.10	POL	526	95	95	LAQFTSAICSVVRRRA	3760
	1186.04	POL	534	95	95	CSVVRRAPPHCLAFS	3761
	F107.05	POL	538	95	95	RRAPPHCLAFSYMDD	3762
	1186.02	POL	546	90	90	AFSYMDDVVLGAKSV	3763
	1186.05	POL	629	85	85	DWKVCQRIVGLLGA	3764
	1280.21	POL	637	95	95	VGLLGAAPFTQCGY	3765
	27.0278	POL	643		95	AAPFTQCGYPALMPL	3766
	1186.21	POL	648	95	95	QCGYPALMPLYACIQ	3767
	1280.14	POL	694	95	95	LCQVFADATPTGWGL	3768
	27.0282	POL	750	85	85	SVVLSRKYTSFPWLL	3769
		X	13	95	90	RDVLCRLPVGAESRG	3770
	1186.07	X	50	95	90	GAHLSRLGPLVCAFS	3771
	1186.29	X	60	95	90	VCAFSSAGPCALRFT	3772
Algorithm	1280.20	ENV	330	100	80	SVRFWSLLYPFVQ	3773
	1280.19	NUC	28	85	80	RDLLDTASALYREAL	3774
	1298.02	POL	56	90	55	VGNFTGLYSSTVPVF	3775
	1298.03	POL	571	95	75	TNFLSLGIHLNPNK	3776
	1298.05	POL	651	95	55	YPALMPLYACIQSKQ	3777
	1298.06	POL	664	95	60	KQAFIFSPTYKAFLC	3778
	1280.181	POL	722	85	80	PLPIHTAELLAACFA	3779
	1280.09	POL	774	90	80	GTSFVYVPSALNPAD	3780
DR3-motif	795.05	ENV	10		95	PLGFFPDHQLDP	3781
	35.0090	ENV	312	95	90	FLLVLLDYQGMLPVC	3782
	CF-03	NUC	28	85	80	RDLLDTASALYREALSPEH	3783
	35.0091	POL	18	90	65	AGPLEEELPRLADEG	3784
	35.0092	POL	34	100	85	NRRVAEDNLGNLNV	3785
	35.0093	POL	96	85	60	VGPLTVNEKRRLKLI	3786
	35.0094	POL	120	100	100	TKYLPLDKGIKPYYP	3787
	35.0095	POL	371	100	55	GGVFLVDKNPHNTTE	3788
	35.0096	POL	385	100	45	ESRLVVDVSQFSRGN	3789
	1186.18	POL	422	95	85	NLSWLSLDVSAAFYH	3790
	35.0099	POL	666	95	55	AFTFSPTYKAFLCKQ	3791
	35.0101	X	18	95	35	LRPVGAESGRPVSG	3792
Lower conservancy or miscellaneous	799.01	ENV	11	80	75	PLLVLQAGFFLLTRILTIQ	3793
	799.02	ENV	31	95		SLDSWWTSLNFLGGTTVCLG	3794
	799.04	ENV	71	95	75	GYRWMCLRRFIIFLLLC	3795

Table XXXIII. Candidate HBV-derived HTL epitopes

Selection criteria	Peptide	Mol	1st Pos	Conservancy		Sequence	SEQ ID NO:
				Core	Total		
	1298.01	ENV	117	80	40	PQAMQWNSTTFHQTL	3796
	1280.06	ENV	180	80	80	AGFFLLTRILTIPQS	3797
	1280.11	ENV	245	80	80	IFLFILLCLIFLLV	3798
	CF-08	NUC	120		90	VSFGVWIRTPPAYRPPNAPI	3799
	1186.25	NUC	121	95	90	SFGVWIRTPPAYRPP	3800
	1280.15	POL	501	80	80	LHLYSHPIILGFRKI	3801
	1298.04	POL	618	80	45	KQCFRKLPVNRPIDW	3802
	1298.07	POL	767	80	70	AANWILRGTSFVYVP	3803
	1298.08	POL	827	80	60	PDRVHFASPLHVAWR	3804

Table XXXIV. HLA-DR screening panels

Screening Panel	Antigen	Representative Assay			Phenotypic Frequencies				
		Alleles	Allele	Alias	Cauc.	Blk.	Jpn.	Chn.	Hisp.
Primary	DR1	DRB1*0101-03	DRB1*0101	(DR1)	18.5	8.4	10.7	4.5	10.1
	DR4	DRB1*0401-12	DRB1*0401	(DR4w4)	23.6	6.1	40.4	21.9	29.8
	DR7	DRB1*0701-02	DRB1*0701	(DR7)	26.2	11.1	1.0	15.0	16.6
	Panel total				59.6	24.5	49.3	38.7	51.1
Secondary	DR2	DRB1*1501-03	DRB1*1501	(DR2w2.01)	19.9	14.8	30.9	22.0	15.0
	DR2	DRB5*0101	DRB5*0101	(DR2w2.02)	-	-	-	-	-
	DR9	DRB1*09011,09012	DRB1*0901	(DR9)	3.6	4.7	24.5	19.9	6.7
	DR13	DRB1*1301-06	DRB1*1302	(DR6w19)	21.7	16.5	14.6	12.2	10.5
	Panel total				42.0	33.9	61.0	48.9	30.5
Tertiary	DR4	DRB1*0405	DRB1*0405	(DR4w15)	-	-	-	-	-
	DR8	DRB1*0801-5	DRB1*0802	(DR8w2)	5.5	10.9	25.0	10.7	23.3
	DR11	DRB1*1101-05	DRB1*1101	(DR5w11)	17.0	18.0	4.9	19.4	18.1
	Panel total				22.0	27.8	29.2	29.0	39.0
Quaternary	DR3	DRB1*0301-2	DRB1*0301	(DR3w17)	17.7	19.5	0.4	7.3	14.4
	DR12	DRB1*1201-02	DRB1*1201	(DR5w12)	2.8	5.5	13.1	17.6	5.7
	Panel total				20.2	24.4	13.5	24.2	19.7
Quaternary	DR3	DRB1*0301-2	DRB1*0301	(DR3w17)	17.7	19.5	0.4	7.3	14.4
	DR12	DRB1*1201-02	DRB1*1201	(DR5w12)	2.8	5.5	13.1	17.6	5.7
	Panel total				20.2	24.4	13.5	24.2	19.7
	Panel total				20.2	24.4	13.5	24.2	19.7

20.4

Table XXXV. HBV-derived cross-reactive HLA-DR binding peptides

Peptide	Mol	1st Pos	Conservancy		Sequence	SEQ ID NO:	HLA-DR binding capacity (IC50 nM)										Total DR alleles bound	
			Core	Total			DR1	DR2w2.01	DR2w2.02	DR3	DR4w4	DR4w15	DR5w11	DR6	DR7	DR8	DR9	
F107.03	POL	412	90	90	LQSLTNLLSSNLSWL	3805	2.0	21	1000	- ^a	9.4	47	294	135	167	557	682	10
1298.06	POL	664	95	60	KQAFTEPTTKAFIC	3806	9.4	38	143	-	41	173	83	175	76	408	139	10
1280.06	ENV	180	80	80	AGFLLTRILTIQPS	3807	1.1	217	1053	-	8.5	253	5.6	9.5	8.1	188	58	9
1280.09	POL	774	90	80	GTSFVYVPSALNPAD	3808	14	650	400	-	118	93	426	-	93	803	221	9
1186.25	NUC	121	95	90	SFGVWIRTPPAYRPP	3809	532	827	47	-	577	603	769	17500	1042	196	938	8
27.0280	NUC	123	95	95	GVWIRTPPAYRPPNA	3810	14	217	2.8	-	13	67	42	-	114	92	1667	8
CF-08	NUC	120	90	90	VSGVWIRTPPAYRPPNAPI	3811	192	105	105	-	300	426	426	-	124	-	-	5
27.0281	POL	145	100	100	RHYLHTLWKAGILYK	3812	17	5.4	35	-	2250	1462	42	745	61	27	174	8
1186.15	ENV	339	95	95	LVPFVQWVFGLSPTV	3813	385	13	1429	-	300	27	53	1944	2717	74	30	7
1280.15	POL	501	80	80	LHLYSHPIILGFRKI	3814	227	268	500	-	66	238	488	17500	-	803	1531	7
F107.04	POL	523	95	95	PFLAQFTSAICSVV	3815	28	337	4762	-	563	317	1667	44	325	845	1271	7
1298.04	POL	618	80	45	KQCFRLKLPVNRPIDW	3816	3.3	4136	952	-	38	45	1538	814	63	845	3000	7
1298.07	POL	767	80	70	AANWILRGTSFYVVP	3817	54	379	3279	-	882	1520	1429	140	43	196	278	7
857.02	NUC	50	90	90	PHHTALRQAILCWGELMTLA	3818	70	9.1	211	-	85	-	263	193000	676	196	2273	7

a. A dash (-) indicates IC50 nM >20,000.

Table XXXVI. HBV-derived DR3-binding peptides

Peptide	Mol	1st Pos	Conservancy		Sequence	SEQ ID NO:	DR3
			Core	Total			
1280.14*	POL	694	95	95	LCQVFADATPTGWGL	3819	67
35.0096	POL	385	100	45	ESRLVVDFSQFSRGN	3820	115
35.0093	POL	96	85	60	VGPLTVNEKRRLKLI	3821	136
1186.27	POL	420	100	85	SSNLSWLSLDVSAAF	3822	200
1186.18	POL	422	95	85	NLSWLSLDVSAAFYH	3823	231

*tested as peptide 35.0100

Table XXXVIIa: HBV Preferred CTL Epitopes

Peptide	Sequence	SEQ ID NO:	Protein	HLA
924.07	FLPSDFFPSV	3824	core 18	A2
777.03	FLLTRILTI	3825	env 183	A2
927.15	ALMPLYACI	3826	pol 642	A2
1013.01	WLSLLVPFV	3827	env 335	A2
1090.77	YMDDVVLGV	3828	pol 538	A2/A1
1168.02	GLSRYVARL	3829	pol 455	A2
927.11	FLLSLGIHL	3830	pol 562	A2
1069.10	LLPIFFCLWV	3831	env 378	A2
1069.06	LLVPFVQWFV	3832	env 338	A2
1147.16	HTLWKAGILYK	3833	pol 149	A3/A1
1083.01	STLPETTVVRR	3834	core 141	A3
1069.16	NVSIPWTHK	3835	pol 47	A3
1069.20	LVVDFSQFSR	3836	pol 388	A3
1090.10	QAFTFSPTYK	3837	pol 665	A3
1090.11	SAICSVVRR	3838	pol 531	A3
1142.05	KVGNGFTGLY	3839	pol 629	A3/A1
1147.05	FPHCLAFSYM	3840	pol 530	B7
988.05	LPSDFFPSV	3841	core 19	B7
1145.04	IPIPSSWAF	3842	env 313	B7
1147.02	HPAAMPHLL	3843	pol 429	B7
26.0570	YPALMPLYACI	3844	pol 640	B7
1147.04	TPARVTGGVF	3845	pol 354	B7
1.0519	DLLDTASALY	3846	core 419	A1
2.0239	LSLDVSAAFY	3847	pol 1000	A1
1039.06	WMMWYWGPSLY	3848	env 359	A1
20.0269	RWMCLRRFII	3849	env 236	A24
20.0136	SWLSLLVPF	3850	env 334	A24
20.0137	SWWTSNLFL	3851	env 197	A24
13.0129	EYLVSGVWI	3852	core 117	A24
1090.02	AYRPPNAPI	3853	core 131	A24
13.0073	WFHISCLTF	3854	core 102	A24
20.0271	SWPKFAVPNL	3855	pol 392	A24
1069.23	KYTSFPWLL	3856	pol 745	-A24
2.0181	LYSHPIILGF	3857	pol 492	A24

Table XXXVIIb: HBV Preferred HTL epitopes

Selection Criteria	Peptide	Mol	1st Pos	Conservancy		SEQ ID NO:	Sequence
				Core	Total		
DR supermotif	F107.03	POL	412	90	90	3838	LQSLTNLLSSNLSWL
	1298.06	POL	664	95	60	3859	KQAFIFSPTYKAFLC
	1280.06	ENV	180	80	80	3860	AGFLLTRILTIQOS
	1280.09	POL	774	90	80	3861	GTSFVYVPSALNPAD
	CF-08	CORE	120		90	3862	VSFGVWIRTPPAYRPPNAPI
	27.0281	POL	145	100	100	3863	RHYLHTLWKAGILYK
	1186.15	ENV	339	95	95	3864	LVPFVQWVFGLSPTV
	1280.15	POL	501	80	80	3865	LHLYSHPIILGFRKI
	F107.04	POL	523	95	95	3866	PFLAQFTSAICSVV
	1298.04	POL	618	80	45	3867	KQCFRKLPVNRPIDW
	1298.07	POL	767	80	70	3868	AANWILRGTSFVYVP
	857.02	CORE	50		90	3869	PHHTALRQAILCWGELMTLA
DR3 motif	1280.14	POL	694	95	95	3870	LCQVFADATPTGWGL
	35.0096	POL	385	100	45	3871	ESRLVVDFSQFSRGN
	35.0093	POL	96	85	60	3872	VGPLTVNEKRRLKLI
	1186.27	POL	420	100	85	3873	SSNLSWLSLDVSAAF